

SEQUENCE LISTING

6180768

(1) GENERAL INFORMATION:

- (i) APPLICANT: MAERTENS, GEERT  
STUYVER, LIEVEN
- (ii) TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES  
AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC  
AGENTS
- (iii) NUMBER OF SEQUENCES: 207
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: ARNOLD, WHITE & DURKEE
  - (B) STREET: P.O. BOX 4433
  - (C) CITY: HOUSTON
  - (D) STATE: TEXAS
  - (E) COUNTRY: USA
  - (F) ZIP: 77210-4433
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: Microsoft Word 6.0 / ASCII text output
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/836,075
  - (B) FILING DATE: 21 Apr 1997
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: PCT/EP95/04155
  - (B) FILING DATE: 23 Oct 1995
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: EP 94870166.9
  - (B) FILING DATE: 21 Oct 1994
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: EP 95870076.7
  - (B) FILING DATE: 28 Jun 1995
- (ix) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: KAMMERER, PATRICIA A.
  - (B) REGISTRATION NUMBER: 29,775
  - (C) REFERENCE/DOCKET NUMBER: INNS:004

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 327 base pairs
  - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

```
ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCTCAK      60
GGSGTNNNNN NNCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG      120
GGCCCCAGGN NGGGTGTGCG CGCGACTAGG AAGACTTCCG AGCGGTCACA ACCTCGTGGC      180
AGGCGACAGC CTATCCCCAA GGCTCGYCGG YCCGAGGGCA GGTCCTGGGC TCAGCCCGGG      240
TATCCTTGGC CCCTCTATGG CAATGAGGGC TGCGGGTGGG CGGGNTGGCT CCTGTCCCCC      300
CGCGGCTCTC GGCCCAATTG GGGCCCCC                                     327
```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn
1           5           10           15

Arg Arg Pro Xaa Xaa Xaa Xaa Xaa Pro Gly Gly Gly Gln Ile Val Gly
20           25           30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Xaa Gly Val Arg Ala
35           40           45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro
50           55           60

Ile Pro Lys Ala Xaa Arg Xaa Glu Gly Arg Ser Trp Ala Gln Pro Gly
65           70           75           80
```

Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Xaa Trp  
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro  
100 105

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GACGGCGTGA ACTATGCAAC AGGGAAGTTG CCCGGTTGCT CTTTCTCTAT CTTCTCTTG	60
GCTTTGCTGT CCTGCTTGAC GGTTCCAACK ACCGCTCAG AGGTGCGCAA CGCATCCGGG	120
GTGTATCATG TCACCAACGA CTGTTCCAAC TCGAGCATCA TCTATGAGAT GGACGGTATG	180
ATCATGCACT ACCCAGGGTG CGTGCCCTGC GTTCGGGAGG ATAACCATCT CCGCTGCTGG	240
ATGGCGCTCA CCCCCACGCT TGGGGTCAAA AAYGCTAGTG TCCCCACTRC GGCAATCCGA	300
CGTCACGTCG ACTTGCTTGT TGGGGGNNCC ACGTTCTGTT CCGCTATGTA CGTGGGRGAC	360
CTTTGCGGGT CTGTCTTCCT CGCTGGCCAG CTATTCACCT TTTCACCCCG CATGCACCAT	420
ACAACGCAGG AGTGCAACTG CTCAATC	447

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Asp Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser

1	5	10	15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Xaa Thr Ala	20	25	30
His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp Cys	35	40	45
Ser Asn Ser Ser Ile Ile Tyr Glu Met Asp Gly Met Ile Met His Tyr	50	55	60
Pro Gly Cys Val Pro Cys Val Arg Glu Asp Asn His Leu Arg Cys Trp	65	70	75
Met Ala Leu Thr Pro Thr Leu Ala Val Lys Xaa Ala Ser Val Pro Thr	85	90	95
Xaa Ala Ile Arg Arg His Val Asp Leu Leu Val Gly Xaa Xaa Thr Phe	100	105	110
Cys Ser Ala Met Tyr Val Xaa Asp Leu Cys Gly Ser Val Phe Leu Ala	115	120	125
Gly Gln Leu Phe Thr Phe Ser Pro Arg Met His His Thr Thr Gln Glu	130	135	140
Cys Asn Cys Ser Ile	145		

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCACAG	60
GACGTCAAGN TCCCGGGTGG TGGTCAGATC GTTGGTGGAG TTTACCTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACCAGG AAGACTTCCG AGCGGTCGCA GCCTCGTGAC	180
AGGCGACAGC CTATTCCTAA GGCTCGCCAG TCCGATGGCA GNNCCTGGGC TCAGCCAGGG	240

CATCCCTGGC CCCTCTATGG CAATGAGGGC TCGGATGGG CGGGATGGCT CCTGTCCCCC 300

CGCGGCTCTC GGCCAGTTG GGGCCCC 327

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Xaa Pro Gly Gly Gly Gln Ile Val Gly  
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Asp Arg Arg Gln Pro  
50 55 60

Ile Pro Lys Ala Arg Gln Ser Asp Gly Xaa Xaa Trp Ala Gln Pro Gly  
65 70 75 80

His Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp  
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro  
100 105

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 447 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GACGGCGTGA	ACTATGCAAC	AGGGAATTTG	CCTGGTTGCT	CTTCTCTAT	CTTCCTCTTA	60
GCTTTTCTGT	CCTGCTTGAC	GGTTCCAAC	ACCGCTCATG	AGGTGCGCAA	CGCATCCGGG	120
GTATATCATC	TCACCAATGA	CTGTTCCAAC	TCGAGCATCA	TCTATGAGAT	GAGTGGTATG	180
ATCTTGCACG	CCCCAGGGTG	TGTGCCCTGC	GTTCGGGAGA	ACAACCTCTC	TCGTTGCTGG	240
ATGCCRCTCA	CCCCACGCT	TGCGGTCAA	GACGCTAATG	TCCCTACTGC	GGCAATCCGA	300
CGCCATGTCG	ACTTGCTGGT	TGGGACAGCC	GCGTTTCGTT	CCGCTATGTA	CGTGGGGGAC	360
CTCTGCGGAT	CCGTCTTCCT	TGTCGGCCAG	CTATTCACCT	TTTCACCCCG	CTTGTACCAT	420
ACAACACAGG	AGTGCAACTG	CTCAATC				447

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser
1				5					10					15	
Ile	Phe	Leu	Leu	Ala	Phe	Leu	Ser	Cys	Leu	Thr	Val	Pro	Thr	Thr	Ala
			20					25					30		
His	Glu	Val	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Leu	Thr	Asn	Asp	Cys
		35					40					45			
Ser	Asn	Ser	Ser	Ile	Ile	Tyr	Glu	Met	Ser	Gly	Met	Ile	Leu	His	Ala
	50					55					60				
Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp
65					70					75					80
Met	Xaa	Leu	Thr	Pro	Thr	Leu	Ala	Val	Lys	Asp	Ala	Asn	Val	Pro	Thr
				85					90					95	
Ala	Ala	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	Gly	Thr	Ala	Ala	Phe
			100					105					110		
Arg	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Ser	Val	Phe	Leu	Val

115	120	125
Gly Gln Leu Phe Thr Phe Ser Pro Arg Leu Tyr His Thr Thr Gln Glu		
130	135	140
Cys Asn Cys Ser Ile		
145		

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 223 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ACACCAACCG CCGCCCACAG	60
GACGTCAAGT TCCCGGGCGG TGGCCAGATC GTTGGTGGAG TCTACGTGCT ACCGCGCAGG	120
GGCCCTAGAT TGGGTGTGCG CGCAGCGCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG	180
AGGCGCCAAC CTATTCCCAA GGAGCGCCGA CCCGAGGGCA GGT	223

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 74 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn	
1	5 10 15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly	
20	25 30
Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala	

35

40

45

Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60

Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg  
 65 70

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGCA ACACCAACCG CCGCCCACAG	60
GACGTTAAAT TCCCGGGTGG GGGGCAGATC GTGGGTGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACGAGG AAGACTTCCG AGCGGTCGCA ACCTCGCGGA	180
AGGCGACAGC CTATCCCCAA GGCTCGCCGA CCCGAGGGCA GGTCTTGGGC TCAGCCTGGG	240
TACCCATGGC CCCTCTATGC TAACGAGGGC TGCGGATGGG CGGGATGGCT CCTGTCCCCT	300
CGCGGCTCCC GTCCTAGCTG GGGCCCCAAT GACCCCCGAC GTAGATCACG CAATTTGGGT	360
AAGGTCATCG ATACCCTAAC GTGTGGCTTC GCCGATCTCA TGGGGTACAT TCCGCTCGTC	420
GGCGCCCCCC TAGGGGGCGC TTCCAGAACC CTGNACATG GTGTCCGGGT CCTGGNAGGC	480
GGCGTGATNN NNNNNNNNNN NAACCTTCN GGTGCTCTT TNNCTATCTT CCTCTTGGCN	540
TTACTCTCTT GCCTCACAGT CCCCACCTCT GCCTATGAGG TGCACAGCAC AACCGATGGC	600
TACCATGTCA CTAATGACTG TTCCAACGGC AGCATCGTAT ATGAGGCAAA GGACATCATC	660
CTTACACGCG CTGGGTGNGT GCCCTGCATA CGGGAAGGCA ATATCTCCCG TTGCTGGGTA	720
CCGCTACCCC CCACGCTCGC AGCGCGGATC GCGAACGCTC CCATCGATGA GGTGCGGCGT	780
CACGTCGACC TCCTCGTGGG GGCAGCCGTG TTCTGCTCAG CCATGTACAT TGGGGACCTT	840



TGTGGGGGCG TCTTCCTCGT TGGGCAATTG TTCACCTTCA CGTCCCGGCG GCATTGGACG 900

GTGCAGGACT GTAATTGTTC CATTTACTCT GGCCACATAA CGGGCCACCG NNNNNNNN 957

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn Thr Asn  
1 5 10 15

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
20 25 30

Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
35 40 45

Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
50 55 60

Ile Pro Lys Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly  
65 70 75 80

Tyr Pro Trp Pro Leu Tyr Ala Asn Glu Gly Cys Gly Trp Ala Gly Trp  
85 90 95

Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro  
100 105 110

Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
115 120 125

Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val Gly Ala Pro Leu  
130 135 140

Gly Gly Ala Ser Arg Thr Leu Xaa His Gly Val Arg Val Leu Xaa Gly  
145 150 155 160

Gly Val Xaa Xaa Xaa Xaa Xaa Asn Leu Xaa Gly Cys Ser Xaa Xaa Ile  
165 170 175

Phe Leu Leu Xaa Leu Leu Ser Cys Leu Thr Val Pro Thr Ser Ala Tyr  
180 185 190

Glu Val His Ser Thr Thr Asp Gly Tyr His Val Thr Asn Asp Cys Ser

195	200	205
Asn Gly Ser Ile Val Tyr Glu Ala Lys Asp Ile Ile Leu His Thr Pro		
210	215	220
Gly Xaa Val Pro Cys Ile Arg Glu Gly Asn Ile Ser Arg Cys Trp Val		
225	230	235 240
Pro Leu Thr Pro Thr Leu Ala Ala Arg Ile Ala Asn Ala Pro Ile Asp		
	245	250 255
Glu Val Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Val Phe Cys		
	260	265 270
Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Gly Val Phe Leu Val Gly		
	275	280 285
Gln Leu Phe Thr Phe Thr Ser Arg Arg His Trp Thr Val Gln Asp Cys		
	290	295 300
Asn Cys Ser Ile Tyr Ser Gly His Ile Thr Gly His Xaa Xaa Xaa		
305	310	315

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACCAAAAGAA ATACCAACCG CCGCCCACAG	60
GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGAT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCACGTGGA	180
AGGCGCCAGC CCATCCCTAA AGATCGGNGN GCCACTGGCA GGTCCCTGGGG ACGTCCAGGA	240
TATCCCTGGC CCCTGTATGG GAACGAGGGG CTCGGCTGGG CAGGATGGCT CCTGTCCCCC	300
CGAGGCTCTC	310

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 108 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	
1				5				10					15			
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	
			20					25					30			
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	
		35				40					45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
	50					55					60					
Ile	Pro	Lys	Asp	Arg	Xaa	Ala	Thr	Gly	Arg	Ser	Trp	Gly	Arg	Pro	Gly	
65					70					75				80		
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	
			85					90					95			
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly					
			100					105								

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 579 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

ACGTGCGGNT	NTGCCGACCT	CATGGGGTAC	ATNCCCGTTG	TCGGCGCCCC	GGTGGGCGGG	60
GTNGCCAGGG	CCCTCGCGNA	TGGCGTGCGG	GTCCTGGAGG	ACGGGATAAA	TTATGNAACA	120

GGGAACCTCC CTGGTTGCTC CTTTTCTATC TTCTNGTTGG CTCTTCTGTC TTGTGTCACC 180  
 GTGCCTGTCT CTGNCGTTGA GGTCAAAAAT ACCAGTCAGG CCTATATGGC AACCAACGAC 240  
 TGCTCCAACA ACAGCATCGT ATGGCAATTG GNGGACGCGG TGCTTCATGT TCCTGGATGT 300  
 GTCCCCTGCG AGAATAGCTC CGGTCGGTTC CACTGTTGGA TCCCGATCTC GCCCAACATA 360  
 GCCGTGAGCA AACCTGGTGC TCTACCAAG GGA CTGCGGG CACGCATTGA TGCCGTCGTG 420  
 ATGTCCGCCA CCCTCTGCTC TGCCCTGTAC GTGGGAGATG TGTGCGGCGC AGTGATGATA 480  
 GCTGCACAGG CTTTCATCGT GGCACCGAAG CGCCATTACT TCGTCCAGGA ATGCAATTGC 540  
 TCCATATACC CAGGCCACAT TACAGGTCAT CGCATGGCG 579

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Thr	Cys	Xaa	Xaa	Ala	Asp	Leu	Met	Gly	Tyr	Xaa	Pro	Val	Val	Gly	Ala	1	5	10	15
Pro	Val	Gly	Gly	Xaa	Ala	Arg	Ala	Leu	Ala	Xaa	Gly	Val	Arg	Val	Leu	20	25	30	
Glu	Asp	Gly	Ile	Asn	Tyr	Xaa	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	35	40	45	
Ser	Ile	Phe	Xaa	Leu	Ala	Leu	Leu	Ser	Cys	Val	Thr	Val	Pro	Val	Ser	50	55	60	
Xaa	Val	Glu	Val	Lys	Asn	Thr	Ser	Gln	Ala	Tyr	Met	Ala	Thr	Asn	Asp	65	70	75	80
Cys	Ser	Asn	Asn	Ser	Ile	Val	Trp	Gln	Leu	Xaa	Asp	Ala	Val	Leu	His	85	90	95	
Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Ser	Ser	Gly	Arg	Phe	His	Cys	100	105	110	
Trp	Ile	Pro	Ile	Ser	Pro	Asn	Ile	Ala	Val	Ser	Lys	Pro	Gly	Ala	Leu	115	120	125	

Thr Lys Gly Leu Arg Ala Arg Ile Asp Ala Val Val Met Ser Ala Thr  
 130 135 140  
 Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys Gly Ala Val Met Ile  
 145 150 155 160  
 Ala Ala Gln Ala Phe Ile Val Ala Pro Lys Arg His Tyr Phe Val Gln  
 165 170 175  
 Glu Cys Asn Cys Ser Ile Tyr Pro Gly His Ile Thr Gly His Arg Met  
 180 185 190  
 Ala

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 957 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

ATGAGCACAA ATCCTAAACC TCAAAGAAAA ACTAAAAGAA AACTAACCG TCGCCACAG	60
GACGTTAAGT TCCCGGGCGG CGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGCCAAGG AAGACTTCTG AACGGTCCCA GCCACGTGGA	180
AGGCGCCAGC CCATCCCAA AGATCGGCGC GCCACTGGCA AGTCCTGGGG ACGTCCAGGA	240
TACCCTTGGC CCCTGTACGG GAACGAGGGC CTCGGCTGGG CAGGGTGGCT CCTGTCCCCC	300
CGGGGCTCTC GCCCTCGTG GGGCCCAAAC GACCCCGGC ACAGGTCACG CAACTTGGGT	360
AAGGTCATCG ATACCCTCAC GTGTGGCTTT GSCGACCTCA TGGGGTACAT ACCTGTCGTC	420
GGCGCCCCCTG TGGGCGGCGT TGCCAGAGCC CTCGCGCATG GCGTGCGGGT CCTGGAGGAC	480
GGGATAAATT ATGCAACAGG GAACTTGCCC GGTGCTCCT TTTCTATCTT CTGCTGGCT	540
CTCTTGCTTT GTATCACCGT GCCCGTGTCT GCCATACAGG TTAAGAACAA CAGCCACTTC	600
TACATGGCGA CTAATGACTG TGCCAATGAC AGCATCGTCT GGCAGCTCAG GGACGCGGTG	660

CTCCATGTTC CTGGATGTGT CCCCTGTGAG AGGTCAGGTA ATAGGACCTT CTGTTGGACA	720
GCGGTCTCGC CCAACGTGGC TGTGAGCCGA CCTGGTGCTC TCACTAGAGG TCTGCGGGCT	780
CACATTGATA CCATCGTGAT GTCCGCCACC CTCTGCTCTG CCCTATACAT AGGGGACCTA	840
TGCGGCGCTG TGATGATAGC AGCGCAAGTT GCCGTCGTCT CACCGCAATA CCATACTTTT	900
GTCCAGGAAT GCAACTGCTC CATATACCCA GGCCATATCA CAGGACATCG AATGGNN	957

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	
1				5					10					15		
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	
			20					25					30			
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	
		35					40					45				
Pro	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
		50				55					60					
Ile	Pro	Lys	Asp	Arg	Arg	Ala	Thr	Gly	Lys	Ser	Trp	Gly	Arg	Pro	Gly	
65				70						75				80		
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	
				85					90					95		
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro	
			100					105					110			
Arg	His	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	
			115				120				125					
Gly	Phe	Xaa	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Val	
		130				135					140					
Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	
145					150				155					160		

Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	
				165					170					175		
Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Ile	Thr	Val	Pro	Val	Ser	Ala	Ile	
				180				185					190			
Gln	Val	Lys	Asn	Asn	Ser	His	Phe	Tyr	Met	Ala	Thr	Asn	Asp	Cys	Ala	
		195					200					205				
Asn	Asp	Ser	Ile	Val	Trp	Gln	Leu	Arg	Asp	Ala	Val	Leu	His	Val	Pro	
	210					215					220					
Gly	Cys	Val	Pro	Cys	Glu	Arg	Ser	Gly	Asn	Arg	Thr	Phe	Cys	Trp	Thr	
225					230				235						240	
Ala	Val	Ser	Pro	Asn	Val	Ala	Val	Ser	Arg	Pro	Gly	Ala	Leu	Thr	Arg	
				245					250					255		
Gly	Leu	Arg	Ala	His	Ile	Asp	Thr	Ile	Val	Met	Ser	Ala	Thr	Leu	Cys	
			260					265					270			
Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Ala	Val	Met	Ile	Ala	Ala	
	275					280						285				
Gln	Val	Ala	Val	Val	Ser	Pro	Gln	Tyr	His	Thr	Phe	Val	Gln	Glu	Cys	
	290					295					300					
Asn	Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	His	Arg	Met	Xaa		
305					310					315						

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

GACGGGGTAA ATTATGCAAC AGGGAATCTG CCTGGTTGCT CTTTCTCTAT CTTCTTGTTG	60
GCTCTTCTGT CTTGTGTCAC CGTGCCTGTC TCTGCCGTGC AGGTTAAGAA CACCAGTACC	120
ATGTACATGG CAACCAATGA CTGTTCCAAC AACAGCATCA TCTGGCAAAT GCAGGGCGCG	180

GTGCTTCATG TTCCTGGATG TGTCCCGTGT GAGTTGCAGG GCAATAAGTC CCGGTGCTGG	240
ATACCGGTCA CTCCCAACGT GGCTGTGAAC CAGCCCGGCG CCCTCACTAG GGGCTTGCGG	300
ACGCACATTG ACACCATCGT GATGGTCGCT ACGCTCTGTT CTGCACTCTA CATCGGGGAC	360
GTGTGTGGCG CGGTGATGAT AGCTGCTCAG GTTGTGATTG TCTCGCCGCA ACATCACAAC	420
TTTTCCCAGG ATTGCAATTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	1	5	10	15
Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Val	Thr	Val	Pro	Val	Ser	Ala	20	25	30	
Val	Gln	Val	Lys	Asn	Thr	Ser	Thr	Met	Tyr	Met	Ala	Thr	Asn	Asp	Cys	35	40	45	
Ser	Asn	Asn	Ser	Ile	Ile	Trp	Gln	Met	Gln	Gly	Ala	Val	Leu	His	Val	50	55	60	
Pro	Gly	Cys	Val	Pro	Cys	Glu	Leu	Gln	Gly	Asn	Lys	Ser	Arg	Cys	Trp	65	70	75	80
Ile	Pro	Val	Thr	Pro	Asn	Val	Ala	Val	Asn	Gln	Pro	Gly	Ala	Leu	Thr	85	90	95	
Arg	Gly	Leu	Arg	Thr	His	Ile	Asp	Thr	Ile	Val	Met	Val	Ala	Thr	Leu	100	105	110	
Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Val	Cys	Gly	Ala	Val	Met	Ile	Ala	115	120	125	
Ala	Gln	Val	Val	Ile	Val	Ser	Pro	Gln	His	His	Asn	Phe	Ser	Gln	Asp	130	135	140	
Cys	Asn	Cys	Ser	Ile												145			

(2) INFORMATION FOR SEQ ID NO: 21:



```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
```

ATGAGCACAA	ATCCTAAACC	TCAAAGAAAA	ACCAAAGAA	ACACTAACCG	CCGCCCACAG	60
GACGTTAAGT	TCCCGGGCGG	TGGCCAGATC	GTTGGCGGAG	TATACTTGTT	GCCGCGCAGG	120
GGCCCCCGGT	TGGGTGTGCG	CGCGACGAGG	AAAACCTCCG	AACGGTCCCA	GCCACGTGGG	180
AGGCGCCAGC	CCATCCCTAA	AGATCGGCGC	TCCACTGGCA	AATCCTGGGG	ACGTCCAGGA	240
TACCCTTGGC	CCCTGTATGG	GAACGAGGGC	CTTG GTTGGG	CAGGATGGCT	CTTGTCCCCT	300
CGAGGCTCTC						310

(ii) MOLECULE TYPE: peptide

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Arg	Ser	Leu	Ala
			20					25					30		
Glu	Tyr	Thr	Cys	Ala	Arg	Arg	Gly	Lys	Leu	Arg	Arg	Ser	Ser	Met	Gly
		35					40					45			

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEOUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GACGGGATAA	ACTACGCAAC	AGGGAATCTG	CCCGGTTGCT	CCTTTTCTAT	CTTCTTGCTG	60
GCCTTGCTAT	CCTGTCTCAC	TGTGCCGGCG	TCCGCTGTGC	AGGTCAAGAA	CACCAGCCAC	120
TCTTATATGG	TGACCAATGA	TTGCTCAAAC	AGCAGCATTG	TCTGGCAGCT	TAAGGATGCT	180
GTGCTTCACG	TCCCTGGATG	TGTTCCATGT	GAGAGGCACC	AAAATCAGTC	TCGCTGCTGG	240
ATACCTGTGA	CACCCAATGT	GGCCGTGAGC	CAACCTGGCG	CGCTCACCAG	GGGTTTGCGG	300
ACGCACATTG	ACACCATCGT	TGCGTCTGCT	ACCGTCTGCT	CAGCTTTGTA	TGTGGGCGAC	360
TTCTGCGGCG	CAGTGATGTT	GGTCTCTCAA	TTTTTCATGA	TCTCCCCTCA	GCACCACATC	420
TTCGTCCAGG	ATTGCAACTG	CTCGATA				447

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser
1				5					10					15	
Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala
			20					25					30		
Val	Gln	Val	Lys	Asn	Thr	Ser	His	Ser	Tyr	Met	Val	Thr	Asn	Asp	Cys
		35					40					45			

Ser Asn Ser Ser Ile Val Trp Gln Leu Lys Asp Ala Val Leu His Val  
 50 55 60  
 Pro Gly Cys Val Pro Cys Glu Arg His Gln Asn Gln Ser Arg Cys Trp  
 65 70 75 80  
 Ile Pro Val Thr Pro Asn Val Ala Val Ser Gln Pro Gly Ala Leu Thr  
 85 90 95  
 Arg Gly Leu Arg Thr His Ile Asp Thr Ile Val Ala er Ala Thr Val 1  
 100 105 110  
 Cys Ser Ala Leu Tyr Val Gly Asp Phe Cys Gly Ala Val Met Leu Val  
 115 120 125  
 Ser Gln Phe Phe Met Ile Ser Pro Gln His His Ile Phe Val Gln Asp  
 130 135 140  
 Cys Asn Cys Ser Ile  
 145

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 356 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GACGGGATAA ACTATGCAAC AGGGAACCTG CCTGGTTGCT CCTTTTCTAT CTTCTTACTG	60
GCCCTGCTTT CTTGCATCAC CGTGCCGGTC TCTGCCGTGC AAGTTGCGAA CCGCAGTGGT	120
TCTTACATGG TGACCAATGA TTGCTCGAAC AGCAGCATCG TTTGGCAGCT CGAGGAGGCC	180
GTCCTTCACG TCCCTGGATG TGTTCCCTGT GAGTGGAAGG ACAACACCTC CCGCTGCTGG	240
ATACCGGTCA CCCCTAACAT CGCTGTGAGC CAACCTGGCG CGCTTACCAA GGGCCTGCGG	300
ACACATATTG ACATCATTTGT CGCGTCCGCC ACGTTCTGCT CTGCCTTGTA TGTGGG	356

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

```

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1           5           10           15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Ile Thr Val Pro Val Ser Ala
          20           25           30

Val Gln Val Ala Asn Arg Ser Gly Ser Tyr Met Val Thr Asn Asp Cys
          35           40           45

Ser Asn Ser Ser Ile Val Trp Gln Leu Glu Glu Ala Val Leu His Val
          50           55           60

Pro Gly Cys Val Pro Cys Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp
65           70           75           80

Ile Pro Val Thr Pro Asn Ile Ala Val Ser Gln Pro Gly Ala Xaa Thr
          85           90           95

Lys Gly Leu Arg Thr His Ile Asp Ile Ile Val Ala Ser Ala Thr Phe
          100          105          110

Cys Ser Ala Leu Tyr Val
          115

```

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 310 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

ATGAGCACGA ATCCTAAACC TCAAAGAAAA ACCAAACGTA ACACCAACCG CCGCCCCATG

60

GACGTTAAGT TCCCCGGGTGG TGGCCAGATC GTTGGCGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCCAGGT TGGGTGTGCG CGCGACTCGG AAGACTTCGG AGCGGTCGCA ACCTCGTGGG	180
AGACGCCAAC CTATCCCCAA GGCGCGTCGA TCCGAGGGAA GGTCTTGGGC ACAGCCAGGA	240
TATCCATGGC CTCTTTACGG TAATGAGGGT TGCGGGTGGG CANNATGGCT CTTGTCCCCC	300
CGCGGTTCTC	310

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	1	5	10	15
Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	20	25	30	
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	35	40	45	
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	50	55	60	
Ile	Pro	Lys	Ala	Arg	Arg	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	65	70	75	80
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Xaa	Trp	85	90	95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro	100	105	110	
Arg	Arg	Arg	Ser	Arg												115			

(2) INFORMATION FOR SEQ ID NO: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

```
GACGGGATCA ATTTTGCAAC AGGGAACCTC CCCGGTTGCT CCTTTTCTAT CTTCTCTTG      60
GCACTCCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCATCA ACTATCGCAA TGTCTCGGGC      120
ATTTACTATG TCACCAATGA TTGCCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC      180
ATCTTGCACC TCCCAGGTTG CGTGCCCTGC GTGAGAGAGG GGAATCAGTC ACGTTGCTGG      240
GTAGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG      300
AGTCATGTGG ACTTGATGGT GGGGGCCGCC ACTGTTTGTT CAGCCCTTTA CATCGGGGAT      360
TTRTGTGGYG GCTTGTTCTT AGTCGGTCAG ATGTTCTCTT TCCGACCAAG GCGCCACTGG      420
ACTACTCAAG ATTGCAATTG TTCCATC                                           447
```

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

```
Asp Gly Ile Asn Phe Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1           5           10           15
Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20          25          30
Ile Asn Tyr Arg Asn Val Ser Gly Ile Tyr Tyr Val Thr Asn Asp Cys
35          40          45
Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50          55          60
Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser Arg Cys Trp
65          70          75          80
```

---

Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile Gly Ala Pro Leu  
85 90 95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val  
100 105 110

Cys Ser Ala Leu Tyr Ile Gly Asp Xaa Cys Xa Gly Leu Phe Leu Val  
115 120 125

Gly Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp  
130 135 140

Cys Asn Cys Ser Ile  
145

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

GACGGGATCA ATTATGCAAC AGGGAACCTT CCCGGTTGCT CTTTTTCTAT CTTCTCTTTG	60
GCACTCCTCT CGTGCCTGAC TGTTCCTGCT TCGGCCATTA ACTACCGCAA CACCTCGGGC	120
ATCTACCACG TCACCAATGA CTGCCCAGAC TCGAGCATAG TTTATGAGGC CGACCACCAC	180
ATCTTGACCC TTCCAGGTTG CGTGCCCTGC GTGAGAACTG GGAATCAGTC ACGTTGCTGG	240
GTGGCCCTTA CTCCTACCGT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCTCTGCGG	300
AGTCATGTGG ATCTGATGGT GGGGGCTGCC ACTGTTTGCT CAGCCCTTTA CATCGGGGAT	360
TTGTGTGGCG GCTTGTCTT GGTGGTCAG ATGTTTTCTT TCCGACCACCG ACGCCACTGG	420
ACTGCCCAGG ATTGCAATTG TTCTATC	447

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser
1			5					10						15	
Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala
		20					25					30			
Ile	Asn	Tyr	Arg	Asn	Thr	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys
		35					40					45			
Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Leu	His	Leu
		50				55					60				
Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Gly	Asn	Gln	Ser	Arg	Cys	Trp
65					70					75					80
Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Ile	Gly	Ala	Pro	Leu
				85					90					95	
Glu	Ser	Leu	Arg	Ser	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr	Val
			100					105					110		
Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Gly	Leu	Phe	Leu	Val
		115					120					125			
Gly	Gln	Met	Phe	Ser	Phe	Arg	Pro	Arg	Arg	His	Trp	Thr	Ala	Gln	Asp
		130				135					140				
Cys	Asn	Cys	Ser	Ile											
145															

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 447 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

```
GACGGGATTA ATTATGCAAC AGGGAATCTT CCCGGTTGCT CCTTTTCTAT CTTCCTCTTG      60
GCACTTCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCATTA ACTACCACAA CACCTCGGGC      120
ATCTATCATA TCACCAACGA CTGCCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC      180
ATCTTGCATC TCCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAATCAGTC GAGTTGCTGG      240
GTGGCCCTTA CCCCTACCAT CGCAGCGCCA TACATCGGCG CACCGCTTGA GTCCTTGCGG      300
AGTCATGTGG ATCTGATGGT GGGGGCGGCC ACTGTCTGTT CAGCCCTTTA CATCGGGGAT      360
TTGTGTGGCG GTGCGTTCTT GGTGCGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG      420
ACCACCCAAG ATTGCAACTG CTCCATC                                           447
```

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

```
Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser
1           5           10           15

Ile Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala
20           25           30

Ile Asn Tyr His Asn Thr Ser Gly Ile Tyr His Ile Thr Asn Asp Cys
35           40           45

Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp His His Ile Leu His Leu
50           55           60

Pro Gly Cys Val Pro Cys Val Arg Val Gly Asn Gln Ser Ser Cys Trp
65           70           75           80

Val Ala Leu Thr Pro Thr Ile Ala Ala Pro Tyr Ile Gly Ala Pro Leu
85           90           95

Glu Ser Leu Arg Ser His Val Asp Leu Met Val Gly Ala Ala Thr Val
100          105          110

Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys Gly Gly Ala Phe Leu Val
```

	115	120	125
Gly	Gln Met Phe Ser Phe Arg Pro Arg Arg His Trp Thr Thr Gln Asp		
130		135	140

Cys Asn Cys Ser Ile  
145

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GACGGGATCA ATTATGCAAC AGGGAATATT CCCGGTTGCT CYTTTTCTAT CTCCTTYTG	60
GCACTTCTCT CGTGTCTGAC TGTCCCGCT TCGGCCACTA ACTATCGCAA CGTCTCGGGC	120
ATCTACCATG TCACCAATGA CTGCCCCGAAT TCAAGCATAG TGTATGAGGC CGACCATCAC	180
ATCTTAGCAC TTCCAGGTTG CGTGCCCTGC GTGAGAGTGG GGAACCAGTC ACGCTGCTGG	240
GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACACCGCGG CGCCGCTTGA GTCCCTGCGG	300
AGTCATGTGG ATCTGATGGT GGGAGCTGCC ACTGTTTGTT CAGCCCTTTA CATCGGGGAY	360
TTGTGTGGCG GCTTGTTCTT GGTGGTCAG ATGTTCTCTT TYCAGCCTCG GCGCCACTGG	420
ACTACCCAGG ATTGCAATTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 149 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn	Ile	Pro	Gly	Cys	Xaa	Phe	Ser	
1					5				10					15		
Ile	Phe	Leu	Xaa	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	
		20						25					30			
Thr	Asn	Tyr	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys	
		35					40					45				
Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Leu	Ala	Leu	
		50				55					60					
Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Val	Gly	Asn	Gln	Ser	Arg	Cys	Trp	
65					70					75					80	
Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Thr	Ala	Ala	Pro	Leu	
				85					90					95		
Glu	Ser	Leu	Arg	Ser	His	Val	Asp	Leu	Met	Val	Gly	Ala	Ala	Thr	Val	
			100					105					110			
Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Xaa	Leu	Cys	Gly	Gly	Leu	Phe	Leu	Val	
		115					120						125			
Gly	Gln	Met	Phe	Ser	Xaa	Gln	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Asp	
		130				135					140					
Cys	Asn	Cys	Ser	Ile												
145																

(2) INFORMATION FOR SEQ ID NO: 37:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GACGGGATTA ATTATGCAAC AGGGAAYCTC CCCGGTTGCT CTTTTTCTAT CTCCTCTTG	60
GCACTTCTCT CGTGCCTGAC TGTCCCCGCT TCGGCCACCA ACTACCGCAA TGTCTCGGGC	120
ATTTACCATG TCACCAATGA CTGCCCCGAAT TCAAGCATAG TGTTTGAGGC CGACCATCAC	180

ATCTTGCACC TTCCAGGATG CGTGCCCTGC GTGAAAGAGG GAAATCATTC ACGCTGCTGG	240
GTGGCCCTTA CCCCTACCGT CGCAGCGCCA TACATCGGCG CGCCACTTGA GTCTCTACGG	300
AGTCATGTGG ATGTGATGGT GGGGGCTGCC ACTGTTTGTT CAGCCCTTTA CATCGGGGAT	360
CTGTGCGGTG GCTTGTTCTT GGTGAGTCAG ATGTTCTCTT TCCGACCACG GCGCCACTGG	420
ACTACCCAGG AATGCAATTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Xaa	Leu	Pro	Gly	Cys	Ser	Phe	Ser	1	5	10	15
Ile	Phe	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala	20	25	30	
Thr	Asn	Tyr	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	Cys	35	40	45	
Pro	Asn	Ser	Ser	Ile	Val	Phe	Glu	Ala	Asp	His	His	Ile	Leu	His	Leu	50	55	60	
Pro	Gly	Cys	Val	Pro	Cys	Val	Lys	Glu	Gly	Asn	His	Ser	Arg	Cys	Trp	65	70	75	80
Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Ile	Gly	Ala	Pro	Leu	85	90	95	
Glu	Ser	Leu	Arg	Ser	His	Val	Asp	Val	Met	Val	Gly	Ala	Ala	Thr	Val	100	105	110	
Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Leu	Cys	Gly	Gly	Leu	Phe	Leu	Val	115	120	125	
Gly	Gln	Met	Phe	Ser	Phe	Arg	Pro	Arg	Arg	His	Trp	Thr	Thr	Gln	Glu	130	135	140	
Cys	Asn	Cys	Ser	Ile												145			

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

GACGGGATCA ATTATGCAAC AGGGAACCTC CCCGGTTGCT CTTTCTCTAT CTTCATCCTG	60
GCACTTCTCT CGTGCCTGAC TGTCCCGGCC TCGGCTCAGC ATTATCGGAA TGTCTCGGGC	120
ATTTACCACG TCACCAACGA CTGCCCCGAAC TCCAGCATAG TGTATGAGTC CGACCATCAC	180
ATCTTACACC TACCAGGGTG TGTACCCTGT GTGAAGACTG GGAACACTTC GCGCTGCTGG	240
GTGGCCTTAA CACCTACCGT GGCCGCGCCC ATACTTTCGG CTCCACTTAT GTCCGTACGG	300
CGGCATGTGG ATCTGATGGT GGGTGCAGCT ACCCTATCGT CTGCCCTCTA CGTTGGAGAC	360
CTCTGCGGGG GTGCCTTCCT AGTGGGGCAG ATGTTACCT TCCAGCCGCG TCGCCACTGG	420
ACTGTCCAAG ACTGCAACTG TTCCATC	447

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Asp Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser	
1                    5                    10                    15	
Ile Phe Ile Leu Ala Leu Leu Ser Cys Leu Thr Val Pro Ala Ser Ala	
20                    25                    30	
Gln His Tyr Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp Cys	

35	40	45
Pro Asn Ser Ser Ile Val Tyr Glu Ser Asp His His Ile Leu His Leu		
50	55	60
Pro Gly Cys Val Pro Cys Val Lys Thr Gly Asn Thr Ser Arg Cys Trp		
65	70	80
Val Ala Leu Thr Pro Thr Val Ala Ala Pro Ile Leu Ser Ala Pro Leu		
85	90	95
Met Ser Val Arg Arg His Val Asp Leu Met Val Gly Ala Ala Thr Leu		
100	105	110
Ser Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Ala Phe Leu Val		
115	120	125
Gly Gln Met Phe Thr Phe Gln Pro Arg Arg His Trp Thr Val Gln Asp		
130	135	140
Cys Asn Cys Ser Ile		
145		

(2) INFORMATION FOR SEQ ID NO: 41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 957 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ATACTAACCG TCGCCCTATG	60
GACGTCAAGT TCCCGGGCGG CGGCCAGATC GTTGGTGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCTCGTT TGGGTGTGCG CGCGACGAGA AAGACCTCCG AACGGTCCCA GCCTAGAGGC	180
AGGCGCCAGC CCATACCAAA GGTACGCCAG CCGACAGGCC GTAGCTGGGG TCAACCCGGC	240
TACCCTTGGC CCCTTTATGG CAACGAGGGC TCGGATGGG CGGGATGGCT CCTGTCCCCC	300
CGCGGGTCTC GTCCTAATTG GGGCCCCAAC GACCCCCGGC GAAGGTCCCG CAACTTGGGT	360
AAGGTCATCG ATACCCTTAC ATNCGGNCTA GCCGACCTCA TGGGGTACAT CCCTGTCCTA	420

GGAGGGCCGC TTGGCGGCGT TGC GGCTGCC CTGGCGCATG GCGTTAGGGC AATCGAGGAC 480  
GGGGTCAATT ACGCAACAGG GAATCTTCCT GGTGCTCCT TTTCTATCTT CCTCTTAGCA 540  
CTGTTATCGT GCCTCACTAC ACCAGCCTCA GCAATTCAAG TCAAGAACGC CTCTGGGATC 600  
TACCATCTTA CCAATGACTG CTCGAACAAC AGCATCGTTT TTGAGGCGGA GACCATGATA 660  
CTGCATCTTC CAGGTTGTGT CCCATGTATC AAGGCGGGGA ATGAGTCACG ATGTTGGCTC 720  
CCTGTCTCCC CCACCTTAGC CGTCCCCAAC TCATCAGTGC CAATCCACGG GTTTCGCCGA 780  
CACGTAGACC TCCTCGTTGG GGCAGCGGCA TTTGTTCGG CCATGTACAT CGGAGACCTC 840  
TGTGGTAGCA TAATCTTGGT AGGGCAGCTT TTTACTTTCA GGCCTAAGTA CCATCAGGTT 900  
ACCCAGGATT GTAAC TGCTC TATNAACNCT GGCCACGTCA CGGGACACAG GATGGCA 957

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 319 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
			35				40					45			
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
			50			55					60				
Ile	Pro	Lys	Val	Arg	Gln	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly
65					70				75					80	
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp
			85					90					95		
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
			100					105					110		
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Xaa

115	120	125
Xaa Leu Ala Asp Leu Met Gly Tyr Ile Pro Val Leu Gly Gly Pro Leu		
130	135	140
Gly Gly Val Ala Ala Ala Leu Ala His Gly Val Arg Ala Ile Glu Asp		
145	150	155 160
Gly Val Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile		
	165 170	175
Phe Leu Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Ile		
	180 185	190
Gln Val Lys Asn Ala Ser Gly Ile Tyr His Leu Thr Asn Asp Cys Ser		
	195 200	205
Asn Asn Ser Ile Val Phe Glu Ala Glu Thr Met Ile Leu His Leu Pro		
	210 215	220
Gly Cys Val Pro Cys Ile Lys Ala Gly Asn Glu Ser Arg Cys Trp Leu		
225	230 235	240
Pro Val Ser Pro Thr Leu Ala Val Pro Asn Ser Ser Val Pro Ile His		
	245 250	255
Gly Phe Arg Arg His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys		
	260 265	270
Ser Ala Met Tyr Ile Gly Asp Leu Cys Gly Ser Ile Ile Leu Val Gly		
	275 280	285
Gln Leu Phe Thr Phe Arg Pro Lys Tyr His Gln Val Thr Gln Asp Cys		
	290 295	300
Asn Cys Ser Xaa Asn Xaa Gly His Val Thr Gly His Arg Met Ala		
305	310 315	

(2) INFORMATION FOR SEQ ID NO: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ACACCATCCG CCGCCCACAG	60
GACGTCAAGT TCCCGGGTGG CGGCCAGATC GTTGGTGGAG TCTACTTGCT GCCGCGCAGG	120
GGCCCGCGCT TGGGTGTGCG CGCGACGAGA AAGACTTCTG AACGGTCCCA GCCCAGAGGT	180
AGGCGCCAAC CAATACCCAA AGTGCGCCAC CAAACGGGCC GTACCTGGGC CCAGCCCGGG	240
TACCCCTGGC CTCTTTATGG AAATGAGGGC TGTGGTTGGG CAGGCTGGCT CCTGTCCCCC	300
CGCGGCTCTC GCCCAAATTG GGGCCCAAAC GACCCCGGC GGAGGTCCCG CAACTTGGGT	360
AAAGTCATCG ACACCCTTAC TTGCGGCTTC GCCGACCTCA TGGGGTATAT CCCTGTCGTA	420
GGCGCTCCGW TGGGAGGCGT CGCGGNGGCC TTGGCGCATG GGGTCANGGN CATCGAGGAC	480
GGNGTAAATT ACGCAACAGN GAATCTTCCC GGMNGCTCTN TCTCTATCTT NCTCTTGGCA	540
CTTCTCTCGT GCCTTACAAC ACCAGCCTCC GCGGCGCATT ATACCAACAA GTCTGGCCTG	600
TACCATCTCA CCAACGACTG CCCCACAGC AGCATCGTTT ATGAGGCGGA GAACTGATT	660
TTGCACTTGC CTGGGTGTGT ACCTTGTGTG AAGRTGRACA ATCAATCCCG GTGCTGGGTG	720
CAGGCCTCCC CGACCCTGGC AGTGCCGAAC GCGTCTACGC CAGTCACCGG GTTCCGAAA	780
CATGTGGACA TCATGGTGGG CGCTGCCGCG TTCTGTTCAG CTATGTATGT GGGGGACCTG	840
TGCGGGGGCC TTTTCCTCGT TGGACAGCTC TTCACGCTCA GGCCTCGGAT GCATCAGGTT	900
GTCCAGGAGT GTAAGTGTTC CATCTACACA GGGCATATCA CTGGACACCG AATGGCA	957

(2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Ile
1				5					10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala

35					40					45					
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
50						55					60				
Ile	Pro	Lys	Val	Arg	His	Gln	Thr	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly
65					70					75				80	
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp
				85					90					95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
			100					105					110		
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys
			115				120					125			
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Xaa
	130					135					140				
Gly	Gly	Val	Ala	Xaa	Ala	Leu	Ala	His	Gly	Val	Xaa	Xaa	Ile	Glu	Asp
145					150					155				160	
Xaa	Val	Asn	Tyr	Ala	Thr	Xaa	Asn	Leu	Pro	Xaa	Xaa	Ser	Xaa	Ser	Ile
				165				170						175	
Xaa	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Leu	Thr	Thr	Pro	Ala	Ser	Ala	Ala
			180					185					190		
His	Tyr	Thr	Asn	Lys	Ser	Gly	Leu	Tyr	His	Leu	Thr	Asn	Asp	Cys	Pro
		195					200					205			
Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Glu	Thr	Leu	Ile	Leu	His	Leu	Pro
	210					215					220				
Gly	Cys	Val	Pro	Cys	Val	Lys	Xaa	Xaa	Asn	Gln	Ser	Arg	Cys	Trp	Val
225					230					235				240	
Gln	Ala	Ser	Pro	Thr	Leu	Ala	Val	Pro	Asn	Ala	Ser	Thr	Pro	Val	Thr
				245					250					255	
Gly	Phe	Arg	Lys	His	Val	Asp	Ile	Met	Val	Gly	Ala	Ala	Ala	Phe	Cys
			260					265					270		
Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	Gly	Gly	Leu	Phe	Leu	Val	Gly
	275						280					285			
Gln	Leu	Phe	Thr	Leu	Arg	Pro	Arg	Met	His	Gln	Val	Val	Gln	Glu	Cys
	290					295					300				
Asn	Cys	Ser	Ile	Tyr	Thr	Gly	His	Ile	Thr	Gly	His	Arg	Met	Ala	
305					310					315					

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 413 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

ATGAGCACAC TTCCTAAACC TCAAAGAAAA ACCAAACGAA ACACCAACCG TCGCCCACAG	60
GACGTCAAGT TCCCGGGTGG CGGTCAGATC GTTGGTGGAG TTTACTTGTT GCCGCGCAGG	120
GGCCCTCGTT TGGGTGTGCG CGCGACGAGG AAAACTTCTG AACGGTCCCA GCCCAGGGGT	180
AGACGCCAAC CTATACCGAA GGTGCGTCAC CAAACGGGCC GTACCTGGGC TCAACCCGGG	240
TACCCCTGGC CTCTTTATGG GAATGAGGGT TGTGGCTGGG CAGGGTGGCT CCTGTCCCCC	300
CNCGGCTCTC GCCCTAATTG GGGCCCTAAT GACCCCCGGN GGAGGTCCCG CAACCTGGGT	360
AAGGTCATCG ATACCCTTAC TTGNGGSTTC GCCGACCTCA TAGAGTACAT TCC	413

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 137 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25					30		
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala
		35					40					45			
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro

50		55		60											
Ile	Pro	Lys	Val	Arg	His	Gln	Thr	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly
65					70					75					80
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp
				85					90					95	
Leu	Leu	Ser	Pro	Xaa	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
			100					105					110		
Arg	Xaa	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Xaa
		115					120					125			
Xaa	Phe	Ala	Asp	Leu	Ile	Glu	Tyr	Ile							
130						135									

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 957 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ATGAGCACAC TTCCAAAACC CCAAAGAAAA ACCAAAAGAA ACACAAACCG TCGCCCAATG	60
GATGTCAAGT TCCCGGGCGG CGGTCAGATC GTTGGTGGAG TCTACTTGTT ACCGCGCAGG	120
GGCCCACGTT TGGGTGTGCG CGCGACGAGG AAGACTTCGG AACGGTCCCA GGCCAGAGGT	180
AGGCGCCAAC CAATACCCAA GGTGCGCCAG AACCAAGGCC GAACCTGGGC TCAGCCTGGG	240
TACCCCTGGC CCCTTTATGG GAACGAGGGC TCGGGCTGGG CGGGGTGGCT CTTGTCCCCC	300
CGTGGCTCTC GCCCGGACTG GGGNCCCAAT GACCCCCGGN GGAGGTCCCG CAACCTGGGT	360
AAGGTCATCG ACACCCTCAC TTGCGGCTTC GCCGACCTCA TGGAGTACAT CCCTGTCGTT	420
GGCGCCCCC TTGGAGGCGT TCGGGCGGAA CTGGNACATG GTGTCAGGGC CATCGAGGAC	480
GGGATAAACT ATGCAACAGG GAATCTTCCT GGTGCTCTT TCTCTATCTT CCWCTTGGCA	540
CTTCTCTCGT GCCTCACCAC GCCTGCCTCC GCACTAAACT ATGCTAACAA GTCTGGGCTG	600

TATCATCTAA CCAATGACTG CCCCAATAGC AGCATTGTGT ATGAGGCGAA TGGCATGATC	660
CTGCATCTCC CGGGTTGCGT CCCCTGCGTG AAGACCGGCA ACCTGACCAA GTGTTGGCTG	720
TCGGCCTCCC CGACATTGGC GGTGCAGAAT GCGTCGGTGT CCATCAGGGG TGTCCGCGAG	780
CACGTGGACC TCTTGGTGGG TGCTGCTGCG TTCTGCTCTG CCATGTACGT GGGCGACTTA	840
TGCGGTGGGC TCTTTCTCGT TGGGCAGTTG TTCACGTTCA GACCCAGGAT GTATGAGATC	900
GCCCAGGACT GCAACTGTTC CATCTATGCA GGCCACATCA CTGGGCACCG GATGGCG	957

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn	1	5	10	15
Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	20	25	30	
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	35	40	45	
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Ala	Arg	Gly	Arg	Arg	Gln	Pro	50	55	60	
Ile	Pro	Lys	Val	Arg	Gln	Asn	Gln	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	65	70	75	80
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	85	90	95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asp	Trp	Xaa	Pro	Asn	Asp	Pro	100	105	110	
Arg	Xaa	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	115	120	125	
Gly	Phe	Ala	Asp	Leu	Met	Glu	Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Leu	130	135	140	
Gly	Gly	Val	Ala	Ala	Glu	Leu	Xaa	His	Gly	Val	Arg	Ala	Ile	Glu	Asp				

145		150		155		160
Gly Ile Asn Tyr Ala Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile						
	165		170		175	
Phe Xaa Leu Ala Leu Leu Ser Cys Leu Thr Thr Pro Ala Ser Ala Leu						
	180		185		190	
Asn Tyr Ala Asn Lys Ser Gly Leu Tyr His Leu Thr Asn Asp Cys Pro						
	195		200		205	
Asn Ser Ser Ile Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu Pro						
	210		215		220	
Gly Cys Val Pro Cys Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu						
	225		230		235	240
Ser Ala Ser Pro Thr Leu Ala Val Gln Asn Ala Ser Val Ser Ile Arg						
	245		250		255	
Gly Val Arg Glu His Val Asp Leu Leu Val Gly Ala Ala Ala Phe Cys						
	260		265		270	
Ser Ala Met Tyr Val Gly Asp Leu Cys Gly Gly Leu Phe Leu Val Gly						
	275		280		285	
Gln Leu Phe Thr Phe Arg Pro Arg Met Tyr Glu Ile Ala Gln Asp Cys						
	290		295		300	
Asn Cys Ser Ile Tyr Ala Gly His Ile Thr Gly His Arg Met Ala						
	305		310		315	

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 309 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

ATGAGCACAC TTCCTAAACC ACAAAGAAAA ACCAAAAGAA ACACCAACCC CGGCCACAGG	60
ACGTTAAGTT CCCAGGCGGC GGTCAGATCG TTGGTGGAGT TTACGTGCTA CCACGCAGGG	120

GCCCCAGTT GGGTGTGCGT GCAGTGCGCA AGACTTCCGA GCGGTCGCAA CCTCGCAGTA 180  
 GCGGCCAACC CATCCCCAGG GCGCGCCGAA CCGAGGGCAG GTCCTGGGCT CAGCCCCGGT 240  
 ACCCTTGGCC CCTATATGGG AATGAGGGCT GCGGGTGGGC AGGGTGGCTC CTGTCCCCGC 300  
 GCGGCTCTC 309

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 115 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	
Xaa	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25					30		
Gly	Val	Tyr	Val	Leu	Pro	Arg	Arg	Gly	Pro	Gln	Leu	Gly	Val	Arg	Ala
		35					40					45			
Val	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Ser	Arg	Arg	Gln	Pro
		50				55					60				
Ile	Pro	Arg	Ala	Arg	Arg	Thr	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly
65					70					75				80	
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp
			85						90					95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
			100					105					110		
Arg	Arg	Arg													

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 447 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA





	85		90		95
Ala Ser Leu Arg Thr His Val Asp Met Met Val Xaa Ala Ala Thr Leu					
	100		105		110
Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Ala Leu Phe Leu Xaa					
	115		120		125
Gly Gln Gly Phe Ser Trp Arg His Arg Gln His Trp Thr Val Gln Asp					
	130		135		140
Cys Asn Cys Ser Ile					
145					

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

CTCGACAGTT ACTGAGAATG ACATCCGTGT CGAGGAATCA ATATACCAAT GTTGTGACTT	60
GGCCCCCGAG GCTCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTACA TCGGGGGCCC	120
YCTAACCAAT TCAAAAGGAC AGAACTGCGG CTACCGTCGG TGCCGCGCCA GCGGCGTGCT	180
GACTACCAGC TGCGGCAACA CCCTGACATG CTACTTGAAA GCCAGAGCGG CCTGTCGAGC	240
TGCAAAGCTC CGGGACTGCA CCATGCTCGT GTGCGGGGAT GACCTTGTCG TTATCTGTGA	300
GAGTGCGGGA GTCGAGGAAG ACGCGGCGAA CCTACGAGCT	340

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln  
1 5 10 15  
Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr  
20 25 30  
Glu Arg Leu Tyr Ile Gly Gly Xaa Leu Thr Asn Ser Lys Gly Gln Asn  
35 40 45  
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys  
50 55 60  
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala  
65 70 75 80  
Ala Lys Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95  
Val Ile Cys Glu Ser Ala Gly Val Glu Glu Asp Ala Ala Asn Leu Arg  
100 105 110  
Ala

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CTCGACAGTT ACTGAGAACG ACATCCGTAC CGAGGRATCA ATCTATCAAT GTTGTGACTT 60  
GGCCCCYGAG GCCCGCAAGG CCATAAAGTC GCTCACCGAG CGGCTGTACG TCGGGGGCCC 120  
CCTAACCAAT TCAAAGGGGC AGAACTGCGG CTATCGTCGG TGTCGCGCTA GCGGCGTGCT 180  
GACCACCAGC TGC GGCAACA CCCTCACATG CTACTTGAAA GCCAGGGCGG CCTGTCGAGC 240  
TGCAAAGCTC CAGGACTGCA CGATGCTCGT GTGCGGAGAC GACCTTGTCG TTATCTGTGA 300

---

## (2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

Ser	Thr	Val	Thr	Glu	Asn	Asp	Ile	Arg	Thr	Glu	Xaa	Ser	Ile	Tyr	Gln
1				5					10					15	
Cys	Cys	Asp	Leu	Ala	Xaa	Glu	Ala	Arg	Lys	Ala	Ile	Lys	Ser	Leu	Thr
			20					25					30		
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	Gln	Asn
			35				40					45			
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Cys
			50				55				60				
Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Arg	Ala	Ala	Cys	Arg	Ala
65					70				75					80	
Ala	Lys	Leu	Gln	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
				85					90					95	
Val	Ile	Cys	Glu	Ser	Ala	Gly	Val	Glu	Glu	Asp	Ala	Ala	Asn	Leu	Arg
			100					105					110		

Val

## (2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

```
CTCGACAGTT ACTGAGAACG ACATTCGTGT CGAGGAATCA ATCTACCAGT GCTGTGACTT      60
GGCCCCCGAG GCCCCGAAGG CCATAAAGTC GCTCACCGAG CGGCTGTATA TCGGGGGTCC      120
CCTAACCAAC TCAAAAGGGC AGAACTGCGG CTACCGTCGG TGCCGCGCCA GCGGCGTGCT      180
GACTACCAGC TGCGGTAATA CCCTCACATG TTACTTGAAA GCCAGGGCGG CCTGTGAGC      240
TGCGAAGCTC CAGGACTGCA CAATGCTCGT GTGCGGAGAC GACCTTGTCG TTATCTGTGA      300
GAGTGCRGGA GTCGAGGAGG ATGCGGCGAA CCTACGAGTC      340
```

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

```
Ser Thr Val Thr Glu Asn Asp Ile Arg Val Glu Glu Ser Ile Tyr Gln
1           5           10           15

Cys Cys Asp Leu Ala Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr
20          25          30

Glu Arg Leu Tyr Ile Gly Gly Pro Leu Thr Asn Ser Lys Gly Gln Asn
35          40          45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Cys
50          55          60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Arg Ala Ala Cys Arg Ala
65          70          75          80

Ala Lys Leu Gln Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
85          90          95

Val Ile Cys Glu Ser Xaa Gly Val Glu Glu Asp Ala Ala Asn Leu Arg
100         105         110

Val
```

(2) INFORMATION FOR SEQ ID NO: 59:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 652 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG	60
TACACCGGAA TTGCCAGGAC GACCGGGTCC TTTCTTGAT CAACCCGCTC AATGCCTGGA	120
GATTTGGGCG TGCCCCCGCA AGACTGCTAG CCGAGTAGTG TTGGGTCGCG AAAGGCCTTG	180
TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCgggGAGG TCTCGTAGAC CGTGCACCAT	240
GAGCACGAAT CCTAAACCTC AAAGAAAAAC CAAAAGAAAC ACCAACCGCC GCCCACAGGA	300
CGTCAAGTTC CCGGGCGGTG GCCAGATCGT TGGTGGAGTC TACGTGCTAC CGCGCAGGGG	360
CCCTAGATTG GGTGTGCGCG CAGCGCGGAA GACTTCGGAG CGGTCGCAAC CTCGTGGGAG	420
GCGCCAACCT ATTCCCAAGG AGCGCCGACC CGAGGGCAGG TCCTGGGCGC AGCCCGGGTA	480
CCCCTGGCCC CTCTATGGTA ACGAGGGCTG CGGGTGGGCA GGTNGGCTCC TGTCCCCTCG	540
CGGCTCCCGT CCTAGTTGGG GTCCTACTGA CCCCCGGCGT AGGTCACGCA ATTTGGGTAA	600
GGTCATCGAT ACCCTCACGT GTTGNTTCGC CGACCTCATG GGTACATAC CG	652

(2) INFORMATION FOR SEQ ID NO: 60:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 138 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5					10					15	

Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly  
 20 25 30  
 Gly Val Tyr Val Leu Pro Arg Arg Gly Pro Arg Leu Gly Val Arg Ala  
 35 40 45  
 Ala Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro  
 50 55 60  
 Ile Pro Lys Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly  
 65 70 75 80  
 Tyr Pro Trp Pro Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Xaa  
 85 90 95  
 Leu Leu Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro  
 100 105 110  
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu Thr Cys  
 115 120 125  
 Xaa Phe Ala Asp Leu Met Gly Tyr Ile Pro  
 130 135

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CTCAACGGTC ACTGAAGCTG ATATCCGAAC AGAGGAGTCC ATATACCAAT GCTGTGACCT	60
GCACCCCGAA GCACGTGTAG CCATCAAGTC TTTGACTGAA AGGCTGTACG TCGGGGGGCC	120
CTTGACCAAT TCAAAAGGGG AGAACTGCGG CTATCGCAGA TGCCGTGCCA GCGGCGTCTT	180
GACAACCAGC TCGGGCAACA CCCTCACCTG CTATATCAAG GCCCTAGCAG CCTGTAGAGC	240
TGCCAAGCTC CAGGACTGCA CCATGCTCGT CTGTGGCGAC GACCTGGTCG TGATCTGCGA	300
GAGTGTAGGG ACCCAGGAGG ATGCGGCGAG CCTGCGAGCC	340

(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 113 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

Ser	Thr	Val	Thr	Glu	Ala	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Ile	Tyr	Gln
1				5				10						15	
Cys	Cys	Asp	Leu	His	Pro	Glu	Ala	Arg	Val	Ala	Ile	Lys	Ser	Leu	Thr
			20					25					30		
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	Glu	Asn
		35					40					45			
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Cys
	50					55					60				
Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Ile	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Ala
65					70				75					80	
Ala	Lys	Leu	Gln	Asp	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
				85				90						95	
Val	Ile	Cys	Glu	Ser	Val	Gly	Thr	Gln	Glu	Asp	Ala	Ala	Ser	Leu	Arg
			100					105						110	
Ala															

(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 340 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

NTCAACAGTC	ACTGAGAGTG	ATATCCGTAC	AGAGGAGTCC	ATCTACCAAT	GCTGTGATCT	60
AGACCCCAGAG	GCTCGCAAGG	CCATAAGGTC	CCTCACAGAG	AGGCTTTATA	TCGGGGGTCC	120
CCTGACAAAC	TCAAAGGGC	AGAACTGCGG	CTACCGCCGA	TGCCGTGCAA	GCGGCGTCCT	180
GACGACTAGC	TGCGGCAACA	CCCTCACCTG	TTACATAAAG	GCCAGGGCAG	CCTGTCGAGC	240
TGCGAAGCTC	CAGGATTGCT	CAATGCTCGT	CTGTGGCGAC	GACCTTGTCG	TTATCTGCGA	300
GATCGAGGGG	NTCCANGAGG	ATCCGTCGAN	NNNNNNNNNN			340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEOUENCE CHARACTERISTICS:



(A) LENGTH: 831 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

CGTAGACCGT GCACCATGAG CACGAATCCT AAACCTCAAA GAAAAACCAA ACGTAACATC	60
AACCGCCGCC CACAGGACGT CAAGTTCCCG GGCGGTGGCC AGATCGTCGG TGGAGTTTAC	120
CTGTTGCCGC GCAGGGGCCC TAGATTGGGT GTGCGCGCGA CTAGGAAGAC TTCCGAGCGG	180
TCGCAACCTC GTGGGAGGCG ACAGCCTATC CCCAAGGCTC GCCGATCCGA GGGCAGGTCC	240
TGGGCTCAGC CCGGGTACCC TTGGCCCCCTC TATGGCAATG AGGGCATGGG TTGGGCAGGG	300
TGGCTCCTGT CCCCCATGG CTCCCGGCCT AGTTGGGGCC CTTCAGACCC CCGGCGTAGG	360
TCGCGTAATT TGGGTAAGGT CATCGATACC CTCACATGCG GCTTCGCCGA CCTCATGGGG	420
TACATTCCGC TCGTCGGCGC CCCCTAGGG GGC GTTGCCA GGGCCCTGGC GCAAGGCTTC	480
CGGGATCTAC CACGTCACCA ACGATTGTTC CAATGGGAGC ATTGTGTATG AGGCGGAAGG	540
CATGATCATG CATCTCCCCG GGTGCGTGCC CTGCGTTCGG GAAGGTAATA TCTCTCGTTG	600
CTGGGTACCG TTTTCCCCCA CGCTCGCAGC CAGGAATGCT AGCGTCCCCA CTCAGGCAAT	660
TCGGCGACAC GTCGACTTGC TTGTTGGGGC GGCCACACTC TGTTCTGCTA TGTATGTGGG	720
GGACCTCTGT GGGTCCGTCT TCCTCGTCGG CCAACTGTTC ACCTTCACAW CCCGCCAGNA	780
CTACACAGTG CAAGACTGCA ATTGTTCCAT CTACCCCGGC CATATAACGG G	831

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Ile	Asn	
1				5					10					15		
Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly	
			20					25					30			
Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly	Val	Arg	Ala	
		35					40					45				
Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	
	50					55					60					
Ile	Pro	Lys	Ala	Arg	Arg	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	
65					70					75					80	
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	
			85					90						95		
Leu	Leu	Ser	Pro	His	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Ser	Asp	Pro	
			100					105					110			
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	
			115				120					125				
Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val	Gly	Ala	Pro	Leu	
	130					135					140					
Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	Gln	Gly	Phe	Arg	Asp	Leu			
145					150					155						

(2) INFORMATION FOR SEQ ID NO: 67:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

NNNNNNNGTC	ACTGAGAGTG	ATATCCGTGT	CGAGGARTCA	ATTACCAAT	GCTGTGACCT	60
GGCCCCCGAG	GCTCGCGTAG	CCATAAAGTC	GCTCACTGAG	CGGCTATATG	TCGGGGGCCC	120

TCTCACCAAC TCAAAAGGAC AGAACTGCGG CTATCGCCGG TGCCGTGCGA GCGGTGTGCT 180  
 GACTACTAGC TGCGGTAACA CCCTCACATG CTACCTGAAA GCCGCCGCGG CCTGTGAGC 240  
 TGCAAAGCTC CGGGAATGCA CAATGCTCGT GTGTGGCGAC GACCTCGTCG TTATCTGTGA 300  
 GAGTGCGGGG GTCCAGGAGG ATGCTGCAAG CCTNNNNNNN 340

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

Xaa	Xaa	Val	Thr	Glu	Ser	Asp	Ile	Arg	Val	Glu	Xaa	Ser	Ile	Tyr	Gln
1				5					10					15	
Cys	Cys	Asp	Leu	Ala	Pro	Glu	Ala	Arg	Val	Ala	Ile	Lys	Ser	Leu	Thr
			20					25					30		
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Leu	Thr	Asn	Ser	Lys	Gly	Gln	Asn
			35				40					45			
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Cys
			50			55					60				
Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Ala	Ala	Ala	Cys	Arg	Ala
65					70				75					80	
Ala	Lys	Leu	Arg	Glu	Cys	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
				85				90						95	
Val	Ile	Cys	Glu	Ser	Ala	Gly	Val	Gln	Glu	Asp	Ala	Ala	Ser	Xaa	Xaa
			100				105						110		

Xaa

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CTCGACAGTC ACAGAGAGAG ATATAAGNAC TGAGGAGTCC ATATACCAGG CTTGTTCTT	60
ACCCGAGCAG GCCAGAACTG CCATACACTC ATTGACTGAG AGACTCTACG TAGGAGGGCC	120
CATGATGAAC AGCAAAGGGC AATCCTGCGG ATACAGGCAT TGCCGCGCCA GCGGAGTGCT	180
CACCACCAGT ATGGGGAATA CCATCACGTG CTACATCAAG GCCCTAGCGG CTTGTAAAGC	240
AGCAGGAATA GTGGCCCCCA CCATGCTGGT GTGCGGCGAT GACCTAGTTG TCATCTCAGA	300
GAGTCAGGGA GTCGAGGAGG ACGACCGGAA CCTGANNNNN	340

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

Ser Thr Val Thr Glu Arg Asp Ile Xaa Thr Glu Glu Ser Ile Tyr Gln	
1	5 10 15
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr	
	20 25 30
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser	
	35 40 45
Cys Gly Tyr Arg His Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met	
	50 55 60
Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys Ala	
65	70 75 80
Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val	
	85 90 95
Val Ile Ser Glu Ser Gln Gly Val Glu Glu Asp Asp Arg Asn Leu Xaa	
	100 105 110

Xaa

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 340 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

CTCAACCGTC ACAGAGAGGG ATATAAGAAC TGAGGAGTCC ATATACCTGG CCTGCTCCTT	60
ACCCGAGCAG GCCCGGACTG CCATACATTC ATTAAGTGGAG AGACTTTACG TGGGAGGGCC	120
CATGATGAAC AGCAAAGGGC AGTCCTGCGG ATACAGGCGT TGCCGCGCTA GCGGAGTGCT	180
CACCACCAGT ATGGGGAACA CCATCACGTG TTATGTGAAA GCCCTCGCAG CTTGTAAAGC	240
TGCGGGCATT GTTGCCCCCA CGATGCTGGT GTGCGGCGAT GACCTGGTTG TCATCTCAGA	300
GAGTCAGGGG GCTGAGGAGG ACGAGCGAAA CCTGAGAGTC	340

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 113 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu	
1                    5                    10                    15	
Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr	
20                    25                    30	
Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser	

---

	35		40		45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met						
50		55		60		
Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala						
65		70		75		80
Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val						
	85		90		95	
Val Ile Ser Glu Ser Gln Gly Ala Glu Glu Asp Glu Arg Asn Leu Arg						
	100		105		110	
Val						

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

CTCAACAGTC GCGGAGAGAG ACATCAGGAC CGAGGAGTCC ATTTACCTTG CCTGCTCCTT	60
ACCCGAGCAA GCCCGAACTG CCATACATTC ATTGACTGAG AGACTTTACG TAGGAGGGCC	120
CATGATGAAC AGCAAGGGAC AGTCCTGCGG TTACAGACGT TGCCGCGCCA GCGGAGTGCT	180
CACCACCAGC ATGGGGAATA CCATCACATG CTATGTGAAG GCATTAGCTG CCTGCAAAGC	240
TGCAGGCATC GTTGCTCCCA CGATGCTGGT TTGTGGCGAC GATCTGGTCA TCATCTCAGA	300
GAGTCAGGGA ACCGAGGAGG ATGAGCGGAA CCTGAGAGTC	340

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

```
Ser Thr Val Ala Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Leu
1           5           10           15

Ala Cys Ser Leu Pro Glu Gln Ala Arg Thr Ala Ile His Ser Leu Thr
20           25           30

Glu Arg Leu Tyr Val Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser
35           40           45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser Met
50           55           60

Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys Lys Ala
65           70           75           80

Ala Gly Ile Val Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val
85           90           95

Ile Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg
100          105          110

Val
```

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1195 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

```
CGNACANCCT CCAGGCCCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG      60
TACACCGGAA TTGCCGGGAA GACTGGGTCC TTTCTTGGAT AAACCCACTC TATGCCCCGC      120
CATTTGGGCG TGCCCCGCA AGACTGCTAR CCGAGTAGCG TTGGGTTGCG AAAGGCCTTG      180
```

TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCXXXGAGG TCTCGTAGAC CGTGCATCAT	240
GAGCACAAAT CCTAAACCTC AAAGAAAAAC CAAAAGAAAC ACTAACCGCC GCCCACAGGA	300
CGTTAAGTTC CCGGGCGGTG GCCAGATCGT TGGCGGAGTA TACTTGTTGC CNTGCAGGGG	360
NCCCAGGTNG NGTNTATGCG CAACGANGAA GACTNCCGAA CAGTCCCAGC CACGTGGGAG	420
GCGCCAGCCC ATCCCGAAAG ATCGGNGCAC CACTGGCAAG TCCTGGGGAC GTCCAGGATA	480
TCCCTGGCCC CTGTATGGGA ACGAGGGCCT CGGGTGGGCA GGGTGGCTCC TGTCCCCCCG	540
GGGCTCCCGC CCGTCATGGG GCCCCACGGA CCCCCGGCAT AGGTCGCGCA ACTTGGGTAA	600
GGTCATCGAT ACCCTCACGT NCGGCTTTNC CGACCTCATG GGGTACATTC CCGTCGTTGG	660
CGCCCCAGTA GNGGGCGTCG CCAGAGCTCT CGCGCATGGC GTGAGAGTCC TGGAGGACGG	720
GATAAACTAT GAAACAGGGA ACCTCCCCGG TTGCTCTTTC TCTATCTCCC TCCTTGCTCT	780
TCTGTCCTGA ATTACCGNGC CAGTTTCTGC TGTGGAAATC AAAAACACCA GMAACACATA	840
CATGGTGACT AACGACTGTT CAAACAGYAG CATCACCTGG CAGCTTNNGN NCGCGGTGCT	900
TCACGTTCCCT GGATGCGTCC CCTGTGAACG AGAGGGCAAC AGTTCCCGGT GCTGGATTCC	960
AGTCACGCCC RACGTAKNCG TGAGCCGACC TGGTGCCCTA ACCGAGGGTT TGCATCGCA	1020
CATCGACACC ATCGTAGCGT CCGCAACATT TTGTTCTGCC CTCTACATAG GGGATGTATG	1080
TGGCGCGATA ATGATAGCTG CCAAGTGGT CATCGTCTCG CCGGAGCATC ATCACTTTGT	1140
CCAGGACTGT AACTGTTCCA TCTACCCGGG CCACATAACG GGGCCTCGTA TGTNG	1195

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr	Asn
1				5				10					15		

Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile	Val	Gly
			20					25				30			

Gly	Val	Tyr	Leu	Leu	Xaa	Cys	Arg	Xaa	Pro	Arg	Xaa	Xaa	Xaa	Cys	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



35					40					45					
Thr	Xaa	Lys	Thr	Xaa	Glu	Gln	Ser	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro
50						55					60				
Ile	Pro	Lys	Asp	Arg	Xaa	Thr	Thr	Gly	Lys	Ser	Trp	Gly	Arg	Pro	Gly
65					70					75					80
Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp
				85					90					95	
Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
			100					105					110		
Arg	His	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu	Thr	Xaa
		115					120					125			
Gly	Phe	Xaa	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Val
	130					135					140				
Xaa	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp
145					150					155					160
Gly	Ile	Asn	Tyr	Glu	Thr	Gly	Asn	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile
				165					170					175	
Ser	Leu	Leu	Ala	Leu	Leu	Ser	Ile	Thr	Xaa	Pro	Val	Ser	Ala	Val	Glu
			180					185					190		
Ile	Lys	Asn	Thr	Xaa	Asn	Thr	Tyr	Met	Val	Thr	Asn	Asp	Cys	Ser	Asn
		195					200					205			
Xaa	Ser	Ile	Thr	Trp	Gln	Leu	Xaa	Xaa	Ala	Val	Leu	His	Val	Pro	Gly
	210					215					220				
Cys	Val	Pro	Cys	Glu	Arg	Glu	Gly	Asn	Ser	Ser	Arg	Cys	Trp	Ile	Pro
225					230					235					240
Val	Thr	Pro	Xaa	Val	Xaa	Val	Ser	Arg	Pro	Gly	Ala	Leu	Thr	Glu	Gly
				245					250					255	
Leu	Arg	Ser	His	Ile	Asp	Thr	Ile	Val	Ala	Ser	Ala	Thr	Phe	Cys	Ser
			260					265					270		
Ala	Leu	Tyr	Ile	Gly	Asp	Val	Cys	Gly	Ala	Ile	Met	Ile	Ala	Ala	Gln
	275						280					285			
Val	Val	Ile	Val	Ser	Pro	Glu	His	His	His	Phe	Val	Gln	Asp	Cys	Asn
	290					295					300				
Cys	Ser	Ile	Tyr	Pro	Gly	His	Ile	Thr	Gly	Pro	Arg	Met	Xaa		
305					310					315					

(2) INFORMATION FOR SEQ ID NO: 77:

(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(iii) ANTI-SENSE: NO

ATCCACAGTC	ACTGAAAGAG	ACATCAGAGT	TGAAGAGTCC	GTTTATCTGT	CCTGTTCACT	60
TCCCGAGGAG	GCCCGAGCTG	CCATACACTC	ACTAACTGAG	AGGCTGTACG	TGGGAGGTCC	120
CATGCAGAAC	AGCAAGGGGC	AATCCTGCGG	ATACAGGCGC	TGCCGCGCCA	GCGGGGTGCT	180
CACCACTAGC	ATGGGGGAATA	CTCTCACATG	CTACTTGAAG	GCCCAGGCGG	CCTGCAGGGC	240
CGCGGGCATT	GTTGCACCCA	CAATGCTGGT	GTGTGGCGAC	GACCTGGTCTG	TCATCTCAGA	300
GAGTCAGGGG	ACTGAGAGGG	ACGAGAACAA	CCTGAGACCT			340

(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Val	Glu	Glu	Ser	Val	Tyr	Leu
1				5					10					15	
Ser	Cys	Ser	Leu	Pro	Glu	Glu	Ala	Arg	Ala	Ala	Ile	His	Ser	Leu	Thr
			20					25					30		
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Gln	Asn	Ser	Lys	Gly	Gln	Ser
		35					40					45			
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Met
	50					55					60				

Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Gln	Ala	Ala	Cys	Arg	Ala
65					70				75					80	
Ala	Gly	Ile	Val	Ala	Pro	Thr	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val
			85						90					95	
Val	Ile	Ser	Glu	Ser	Gln	Gly	Thr	Glu	Arg	Asp	Glu	Asn	Asn	Leu	Arg
			100					105					110		
Pro															

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

CTCAACAGTC	ACGGAGAGGG	ACATCAGGAA	TGAGGAGTCC	ATATTCCTGG	CCTGCTCGTT	60
GCCCCGAGGAG	GCCCCGACTG	TCATACATTC	GCTCACTGAG	AGACTCTACA	TAGGCGGGCC	120
GATGATGAAC	AGCAAAGGCC	AGTCCTGTGG	ATACAGGCGT	TGTCGCGCCA	GCGGGGTGTT	180
CACCACTAGC	ATGGGCAATA	CCATCACGTG	CTATGTGAAA	GCCATGGCAG	CTTGCAAGAGC	240
TGCCGGGATT	GACGCCCCCA	CAATGTTGGT	ATGTGGCGAC	GACCTGGTGG	TCATCTCAGA	300
GAGTCAGGGG	ACCGAGGAGG	ACGAGCGAAA	TCTGAGAGTC			340

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

Ser Thr Val Thr Glu Arg Asp Ile Arg Asn Glu Glu Ser Ile Phe Leu  
 1 5 10 15  
 Ala Cys Ser Leu Pro Glu Glu Ala Arg Thr Val Ile His Ser Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Ile Gly Gly Pro Met Met Asn Ser Lys Gly Gln Ser  
 35 40 45  
 Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser Met  
 50 55 60  
 Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Met Ala Ala Cys Arg Ala  
 65 70 75 80  
 Ala Gly Ile Asp Ala Pro Thr Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu Arg Asn Leu Arg  
 100 105 110  
 Val

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CTCTTGACTC TACTGTCACT GAACAGGATA TCAGGGTAGA AGAAGAAATA TACCAATGTT	60
GTGACCTTGA GCCGGAGGCT AGACGGGCAA TCAAATCGCT CACGGAACGG CTTTACGTTG	120
GAGGTCCCAT GTTCAACAGC AAGGGGCTCA AATGCGGATA TCGCCGTTGC CGTGCTAGCG	180
GTGTATTGCC CACTAGCTAC GGTAATACAA TCACCTGCTA CATCAAGGCC AGAGCGGCTG	240
CTCGAGCTGC GGGCCTTCAA GACCCATCAT TCCTTGCTCTG CGGAGATGAT TTGGTGCTAG	300
TGGCTGAGAG TTGCGKCGTT GATGAGGAGG ATAGGGCAGC	340

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

```
Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln
1           5           10           15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Arg Ala Ile Lys Ser Leu Thr
          20           25           30

Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Leu Lys
          35           40           45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Tyr
          50           55           60

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Arg Ala Ala Ala Arg Ala
65           70           75           80

Ala Gly Leu Gln Asp Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
          85           90           95

Val Val Ala Glu Ser Cys Xaa Val Asp Glu Glu Asp Arg Ala Ala Leu
          100          105          110

Arg
```

(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

```
CTCCACTGTA ACCGAAAAGG ACATCAGGCC CGAGGAAGAG GTCTATCAGT GTTGTGACCT      60
GGAGCCCGAA GCTCGCAAGG TTATTACCGC CCTCACAGAA AGACTCTACG TGGGCGGCCC      120
CATGCACAAC AGCAAGGGAG ACCTTTGTGG GTATCGGAGA TGCCGCGCAA GCGGCGTCTA      180
CACGACCAGC TTCGGAAACA CACTGACGTG CTACCTCAAA GCCTCAGCTG CTATTAGAGC      240
GGCAGGGCTG AGAGACTGCA CCATGCTGGT TTGCGGTGAC GACTTGGTCG TCATCGCTGA      300
GAGCGATGGC GTAGAGGAGG ATAACCGAGC CCTCCNAGCC                          340
```

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

```
Ser Thr Val Thr Glu Lys Asp Ile Arg Pro Glu Glu Glu Val Tyr Gln
1           5           10           15

Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Val Ile Thr Ala Leu Thr
          20           25           30

Glu Arg Leu Tyr Val Gly Gly Pro Met His Asn Ser Lys Gly Asp Leu
          35           40           45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe
          50           55           60

Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Ser Ala Ala Ile Arg Ala
65           70           75           80

Ala Gly Leu Arg Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val
          85           90           95

Val Ile Ala Glu Ser Asp Gly Val Glu Glu Asp Asn Arg Ala Leu Xaa
          100          105          110

Ala
```

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CTCCACGGTG ACTGAAAAGG ACATCAGGGT CGAGGAAGAG ATCTATCAAT GTTGTGACCT	60
GGARCCCGAA GCCCGCAAAG CAATATCCGC CCTCACAGAG AGRCTCTACT TGGGCGGCCC	120
CATGTATAAC AGCAAAGGGG AGCTCTGCGG GTATCGGAGG TGCCGCGCGA GCGGAGTGTA	180
CACCACAAGT TTCGGGAACA CAGTGACCTG CTATCTTAAG GCCACCGCAG CTACCAGGGC	240
TGCAGGCCTA AAAGACTGCA CCATGCTGGT CTGCGGTGAC GACTTGGTCG TCATCGCCGA	300
GAGCGAGGGC GTAGAGGAGG ATTCCCAACC CCTCCGAGCC	340

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

Ser Thr Val Thr Glu Lys Asp Ile Arg Val Glu Glu Glu Ile Tyr Gln	
1	5 10 15
Cys Cys Asp Leu Xaa Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr	
	20 25 30
Glu Xaa Leu Tyr Leu Gly Gly Pro Met Tyr Asn Ser Lys Gly Glu Leu	
	35 40 45
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe	
	50 55 60
Gly Asn Thr Val Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala	
65	70 75 80

Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95

Val Ile Ala Glu Ser Glu Gly Val Glu Glu Asp Ser Gln Pro Leu Arg  
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 340 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

CTCCACCGTA ACCGAAAGGG ACATCAGGGT CGAGGAGGAG GTCTATCAGT GTTGTGATCT	60
GGAGCCAGAG GCCCGCAAGG CAATATCCGC CCTCACGGAG AGACTCTATG TGGGCGGTCC	120
CATGTTTAAC AGCAAGGGAG ACCTATGTGG CTACCGCAGG TGCCGCGCAA GCGGCGTCTA	180
CACCACCAGC TTCGGAAACA CACTGACCTG CTACCTCAAG GCCACGGCCG CTACCAGAGC	240
GGCCGGCCTG AAGGATTGCA CAATGCTGGT TTGCGGGGAC GACCTGGTCG TCATCGCAGA	300
GAGCGATGGC GTGGACGAGG ACCGCCGAGC CCTCCAAGCT	340

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 113 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

Ser Thr Val Thr Glu Arg Asp Ile Arg Val Glu Glu Glu Val Tyr Gln



1	5	10	15
Cys Cys Asp Leu Glu Pro Glu Ala Arg Lys Ala Ile Ser Ala Leu Thr			
20	25	30	
Glu Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Asp Leu			
35	40	45	
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Tyr Thr Thr Ser Phe			
50	55	60	
Gly Asn Thr Leu Thr Cys Tyr Leu Lys Ala Thr Ala Ala Thr Arg Ala			
65	70	75	80
Ala Gly Leu Lys Asp Cys Thr Met Leu Val Cys Gly Asp Asp Leu Val			
85	90	95	
Val Ile Ala Glu Ser Asp Gly Val Asp Glu Asp Arg Arg Ala Leu Gln			
100	105	110	
Ala			

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

CTCAACAGTC ACAGAGCGCG ATGTCCAGAC GGAGCATGAC ATCTACCAGT GCTGTAAGTT	60
GGAGCCCGCA GCACGGACAG CCATCACATC GCTTACTGAC CGATTGTACT NCGGTGGTCC	120
CATGTNTAAC TCTAAAGGTC AGGCATGTGG ATACCGTAGG TGCAGGGCCA GTGGCGTCTT	180
GACCACCATC CTGGCCAATA CTCTGACTTG CTAATTGAAA GCTCAGGCGG CATGCAGAGC	240
TGCCGGGCTG AAGGACTTTG ACATGTTGGT CTGCGGAGAC GACCTTGTCG TTATTTTCGGA	300
GAGTTTGGGG GTCTCGGAGG AACTAGTGC ACTGCGAGCT	340

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

Ser Thr Val Thr Glu Arg Asp Val Gln Thr Glu His Asp Ile Tyr Gln  
1 5 10 15

Cys Cys Lys Leu Glu Pro Ala Ala Arg Thr Ala Ile Thr Ser Leu Thr  
20 25 30

Asp Arg Leu Tyr Xaa Gly Gly Pro Met Xaa Asn Ser Lys Gly Gln Ala  
35 40 45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ile Leu  
50 55 60

Ala Asn Thr Leu Thr Cys Tyr Leu Lys Ala Gln Ala Ala Cys Arg Ala  
65 70 75 80

Ala Gly Leu Lys Asp Phe Asp Met Leu Val Cys Gly Asp Asp Leu Val  
85 90 95

Val Ile Ser Glu Ser Leu Gly Val Ser Glu Asp Thr Ser Ala Leu Arg  
100 105 110

Ala

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CTCGACAGTC ACCGAGCGCG ACATCCRCAC CGAGCACGAC ATCTACCAAT GCTGCCAACT	60
TGACCCGGTG GCACGCAAGG CTATTACATC TCTGACTGAG CGGCTGTACT GCGGWGGGCC	120
CATGATGAAC TCCCGTGGTC AATCATGTGG ATACCGTAGG TGCCGAGCCA GTGGCGTGCT	180
CACCACGAGC TTGGGCAATA CCCTAACATG CTATTTGAAA GCACAAGCAG CGTGTAGGGC	240
AGCAAAGCTC AAAAAGTATG ACATGTTAGT CTGCGGAGAC GATCTAGTCG TTATCGCGGA	300
GAGTGGAGGA GTCTCTGAGG ATGTTGACGC CCTGCGAGCA	340

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Xaa	Thr	Glu	His	Asp	Ile	Tyr	Gln	1	5	10	15
Cys	Cys	Gln	Leu	Asp	Pro	Val	Ala	Arg	Lys	Ala	Ile	Thr	Ser	Leu	Thr	20	25	30	
Glu	Arg	Leu	Tyr	Cys	Xaa	Gly	Pro	Met	Met	Asn	Ser	Arg	Gly	Gln	Ser	35	40	45	
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Leu	Thr	Thr	Ser	Leu	50	55	60	
Gly	Asn	Thr	Leu	Thr	Cys	Tyr	Leu	Lys	Ala	Gln	Ala	Ala	Cys	Arg	Ala	65	70	75	80
Ala	Lys	Leu	Lys	Asn	Tyr	Asp	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val	85	90	95	
Val	Ile	Ala	Glu	Ser	Gly	Gly	Val	Ser	Glu	Asp	Val	Asp	Ala	Leu	Arg	100	105	110	
Ala																			

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid

```
(ii) MOLECULE TYPE: cDNA
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
```

CTCCTCCGTC	ACGGAGCGTG	ACATCCGCAC	TGAACACGAC	ATCTATCAGT	GCTGCCAATT	60
AGATCCGGTA	GCACGGAAAG	CCATTACATC	TCTTACTGAG	CGGCTGTACT	GCGGCGGCCC	120
CATGTACAAC	TCTCGAGGTC	AGTCATGTGG	GTACCGCAGG	TGCCGGGCTA	GTGGTGTCTT	180
CACCACAAGC	TTGGGCAACA	CCATGACATG	CTACCTGAAG	GCTCAGGCGG	CTTGTAGGGC	240
AGCRAAGCTC	AAAAACTTTG	ACATGTTGGT	CTGCGGAGAC	GACCTAGTCG	TTATTGCTGA	300
GAGCGGAGGA	GTCCCTGAGG	ATGCCGGGGC	CCTGCGAGTC			340

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

Ser	Ser	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	His	Asp	Ile	Tyr	Gln
1				5					10					15	
Cys	Cys	Gln	Leu	Asp	Pro	Val	Ala	Arg	Lys	Ala	Ile	Thr	Ser	Leu	Thr
			20					25					30		
Glu	Arg	Leu	Tyr	Cys	Gly	Gly	Pro	Met	Tyr	Asn	Ser	Arg	Gly	Gln	Ser
		35					40					45			
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser	Leu
	50					55					60				
Gly	Asn	Thr	Met	Thr	Cys	Tyr	Leu	Lys	Ala	Gln	Ala	Ala	Cys	Arg	Ala
65					70					75					80
Xaa	Lys	Leu	Lys	Asn	Phe	Asp	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val

85

90

95

Val Ile Ala Glu Ser Gly Gly Val Pro Glu Asp Ala Gly Ala Leu Arg  
 100 105 110

Val

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 340 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

ATCCACAGTC	ACGGGGCGCG	ACATACGCAC	AGAACNAGAC	ATTTACCTGT	CCTGCCAGCT	60
CGACCCAGAG	GCCCGGAAAG	CCATAAAGTC	TCTCACTGAG	AGGCTCTATG	TCGGGGGCCC	120
TATGTACAAC	TCAAAGGGCC	AACTCTGTGG	TCAACGCCGA	TGCCGAGCAA	GCGGAGTACT	180
CCCCACAAGC	ATGGGTAACA	CCATCACATG	CTTCCTGAAG	GCAACCGCCG	CTTGCCGAGC	240
AGCCGGCTTT	ACAGATTATG	ACATGTTGGT	CTGCGGAGAC	GATTTGGTTG	TCGTAACTGA	300
GAGTGCTGGA	GTCAACGAGG	ATATCGCTAA	CCTGCGAGCC			340

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 113 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

Ser	Thr	Val	Thr	Gly	Arg	Asp	Ile	Arg	Thr	Glu	Xaa	Asp	Ile	Tyr	Leu
1				5				10					15		

Ser Cys Gln Leu Asp Pro Glu Ala Arg Lys Ala Ile Lys Ser Leu Thr  
 20 25 30  
 Glu Arg Leu Tyr Val Gly Gly Pro Met Tyr Asn Ser Lys Gly Gln Leu  
 35 40 45  
 Cys Gly Gln Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Met  
 50 55 60  
 Gly Asn Thr Ile Thr Cys Phe Leu Lys Ala Thr Ala Ala Cys Arg Ala  
 65 70 75 80  
 Ala Gly Phe Thr Asp Tyr Asp Met Leu Val Cys Gly Asp Asp Leu Val  
 85 90 95  
 Val Val Thr Glu Ser Ala Gly Val Asn Glu Asp Ile Ala Asn Leu Arg  
 100 105 110  
 Ala

(2) INFORMATION FOR SEQ ID NO: 97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CTCCACTGTC ACTGAGCAGG ACATCAGGGT AGAACTTTCC ATCTTTCAGG CCTGTGACCT	60
CAAGGACGAG GCTAGGAGGG TGATAACTTC ACTCACGGAG CGGCTTTACT GTGGTGGTCC	120
TATGTTCAAC AGCAAGGGAC AACACTGCGG TTACCGCCGC TGCCGTGCTA GTGGGGTGCT	180
ACCCACCAGC TTCGGGAACA CAATCACCTG TTACATCAAA GCAAAGGCAG CTACCAAAGC	240
TGCCGGAATT AAAAATCCAT CATTCCTTGT CTGCGGAGAT GACTTGGTCG TGATTGCTGA	300
GAGTGCAGGG ATCGATGAGG ACAAGAGCGC CTTGAGAGCT	340

(2) INFORMATION FOR SEQ ID NO: 98:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

```

Ser Thr Val Thr Glu Gln Asp Ile Arg Val Glu Leu Ser Ile Phe Gln
1           5           10           15

Ala Cys Asp Leu Lys Asp Glu Ala Arg Arg Val Ile Thr Ser Leu Thr
          20           25           30

Glu Arg Leu Tyr Cys Gly Gly Pro Met Phe Asn Ser Lys Gly Gln His
          35           40           45

Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Pro Thr Ser Phe
          50           55           60

Gly Asn Thr Ile Thr Cys Tyr Ile Lys Ala Lys Ala Ala Thr Lys Ala
65           70           75           80

Ala Gly Ile Lys Asn Pro Ser Phe Leu Val Cys Gly Asp Asp Leu Val
          85           90           95

Val Ile Ala Glu Ser Ala Gly Ile Asp Glu Asp Lys Ser Ala Leu Arg
          100          105          110

Ala

```

(2) INFORMATION FOR SEQ ID NO: 99:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CTCTACCGTC ACAGAGAGGG ACATACGGAC AGAAGAATCC ATCTATCTGT CTTGTCAATT







Val Ile Ser Glu Ser Lys Gly Val Glu Glu Asp Gln Arg Asp Leu Xaa  
100 105 110

Xaa

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 461 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

CGTACAGCCT CCAGGACCCC CCCTCCCGGG AGAGCCATAG TGGTCTGCGG AACCGGTGAG	60
TACACCGGAA TTGCCGGGAA GACTGGGTCC TTTCTTGAT TAACCCACTC TATGCCCGGA	120
GATTGGGCG TGCCCCGCA AGACTGCTAG CCGAGTAGCG TTGGGTGCG AAAGGCCTTG	180
TGGTACTGCC TGATAGGGTG CTTGCGAGTG CCCCAGGAGG TCTCGTAGAC CGTGCACCAT	240
GAGCACGAAT CCTAAACCTC AAAGACAAAC CAAAAGAAAC ACCAACCGCC GCCACAGGA	300
CGTTAAGTTC CCGGGCGGTG GCCAGATCGT TGGCGGGGTG TACTTGTGTC CGCGCAGGGG	360
CCCCAGAGTG GGTGTGCGCG CGACGAGAAA GACCTCGGAG CGGTCCCAGC CGCGTGGGAG	420
GCGCCAACCT ATCCCCAAGG TTAGGCGCAC CACCGGCCGT T	461

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

Met Ser Thr Asn Pro Lys Pro Gln Arg Gln Thr Lys Arg Asn Thr Asn

1	5	10	15
Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly Gln Ile Val Gly			
20	25	30	
Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro Arg Val Gly Val Arg Ala			
35	40	45	
Thr Arg Lys Thr Ser Glu Arg Ser Gln Pro Arg Gly Arg Arg Gln Pro			
50	55	60	
Ile Pro Lys Val Arg Arg Thr Thr Gly Arg			
65	70		

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 340 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CTCTACTGTC ACAGAGAGGG ATATACGAAC AGAGGAATCC ATYTATCTGG CTTGTCAATT	60
GCCCGAAGAG GCCCGGAAGG CCATCAAATC ACTGACAGAG AGACTATACG TGGGCGGCCC	120
GATGGAAAAC AGCAAGGGCC AGGCCTGCGG ATACAGGCGT TGCCGCGCAA GCGGGGTATT	180
CACCACAAGC TTGGGGAACA CCATGACTTG TTACATCAAA GCCAAGGCGG CTTGTAAAGC	240
CGCTGGCATT GTTGACCCAG TGATGCTCGT GTGCGGCGAC GACCTAGTGG TCATCTCAGA	300
AAGCAAGGGG GTGGAGGAGG ACCAACGAGA CCTACGANTC	340

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 113 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

Ser	Thr	Val	Thr	Glu	Arg	Asp	Ile	Arg	Thr	Glu	Glu	Ser	Xaa	Tyr	Leu	
1				5				10						15		
Ala	Cys	Gln	Leu	Pro	Glu	Glu	Ala	Arg	Lys	Ala	Ile	Lys	Ser	Leu	Thr	
			20					25					30			
Glu	Arg	Leu	Tyr	Val	Gly	Gly	Pro	Met	Glu	Asn	Ser	Lys	Gly	Gln	Ala	
			35				40					45				
Cys	Gly	Tyr	Arg	Arg	Cys	Arg	Ala	Ser	Gly	Val	Phe	Thr	Thr	Ser	Leu	
	50					55					60					
Gly	Asn	Thr	Met	Thr	Cys	Tyr	Ile	Lys	Ala	Lys	Ala	Ala	Cys	Lys	Ala	
65					70				75					80		
Ala	Gly	Ile	Val	Asp	Pro	Val	Met	Leu	Val	Cys	Gly	Asp	Asp	Leu	Val	
				85				90						95		
Val	Ile	Ser	Glu	Ser	Lys	Gly	Val	Glu	Glu	Asp	Gln	Arg	Asp	Leu	Arg	
			100					105					110			
																Xaa

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

Ala	Arg	Gln	Ser	Asp	Gly	Arg	Ser	Trp	Ala	Gln
1				5				10		

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 11 amino acids  
    (B) TYPE: amino acid  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

Ala Arg Arg Ser Glu Gly Arg Ser Trp Ala Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

Glu Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Ala Arg Arg Pro Glu Gly Arg Ser Trp Ala Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Asp Arg Arg Thr Thr Gly Lys Ser Trp Gly Arg  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

Asp	Arg	Arg	Ala	Thr	Gly	Arg	Ser	Trp	Gly	Arg
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

Asp	Arg	Arg	Ala	Thr	Gly	Lys	Ser	Trp	Gly	Arg
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

Val	Arg	Gln	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

Val	Arg	His	Gln	Thr	Gly	Arg	Thr	Trp	Ala	Gln
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

Val	Arg	Gln	Asn	Gln	Gly	Arg	Thr	Trp	Ala	Gln
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

Ala	Arg	Arg	Thr	Glu	Gly	Arg	Ser	Trp	Ala	Gln
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

---

Val Arg Arg Thr Thr Gly Arg Xaa Xaa Xaa Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 119:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

Val Arg Arg Thr Thr Gly Arg Thr Trp Ala Gln  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 120:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 121:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

His Glu Val Arg Asn Ala Ser Gly Val Tyr His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 122:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Tyr	Glu	Val	His	Ser	Thr	Thr	Asp	Gly	Tyr	His	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 123:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Val	Glu	Val	Lys	Asn	Thr	Ser	Gln	Ala	Tyr	Met	Ala
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 124:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Ile	Gln	Val	Lys	Asn	Asn	Ser	His	Phe	Tyr	Met	Ala
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Val	Gln	Val	Lys	Asn	Thr	Ser	Thr	Met	Tyr	Met	Ala
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val	Gln	Val	Lys	Asn	Thr	Ser	His	Ser	Tyr	Met	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Val	Gln	Val	Ala	Asn	Arg	Ser	Gly	Ser	Tyr	Met	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Val	Glu	Ile	Lys	Asn	Thr	Xaa	Asn	Thr	Tyr	Val	Leu
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 129:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Val	Glu	Ile	Lys	Asn	Thr	Ser	Asn	Thr	Tyr	Val	Leu
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 130:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Ile	Asn	Tyr	Arg	Asn	Val	Ser	Gly	Ile	Tyr	Tyr	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ile	Asn	Tyr	Arg	Asn	Thr	Ser	Gly	Ile	Tyr	His	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Ile	Asn	Tyr	His	Asn	Thr	Ser	Gly	Ile	Tyr	His	Ile
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

Thr	Asn	Tyr	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 134:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

Gln	His	Tyr	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

Ile	Gln	Val	Lys	Asn	Ala	Ser	Gly	Ile	Tyr	His	Leu
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

Ala	His	Tyr	Thr	Asn	Lys	Ser	Gly	Leu	Tyr	His	Leu
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

Leu	Asn	Tyr	Ala	Asn	Lys	Ser	Gly	Leu	Tyr	His	Leu
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

Leu	Glu	Tyr	Arg	Asn	Ala	Ser	Gly	Leu	Tyr	Met	Val
1				5					10		

(2) INFORMATION FOR SEQ ID NO: 139:

---

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

Ile	Tyr	Glu	Met	Asp	Gly	Met	Ile	Met	His	Tyr
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

Ile	Tyr	Glu	Met	Ser	Gly	Met	Ile	Leu	His	Ala
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

Val	Tyr	Glu	Ala	Lys	Asp	Ile	Ile	Leu	His	Thr
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

Val	Trp	Gln	Leu	Xaa	Asp	Ala	Val	Leu	His	Val
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

Val	Trp	Gln	Leu	Arg	Asp	Ala	Val	Leu	His	Val
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

Ile	Trp	Gln	Met	Gln	Gly	Ala	Val	Leu	His	Val
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

---

Val Trp Gln Leu Lys Asp Ala Val Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

Val Trp Gln Leu Glu Glu Ala Val Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

Thr Trp Gln Leu Xaa Xaa Ala Val Leu His Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

Val Tyr Glu Ala Asp His His Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

Val	Tyr	Glu	Ala	Asp	His	His	Ile	Leu	Ala	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

Val	Phe	Glu	Ala	Asp	His	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Val	Tyr	Glu	Ser	Asp	His	His	Ile	Leu	His	Leu
1				5					10	

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Val Phe Glu Glu Thr Met Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Val Tyr Glu Ala Glu Thr Leu Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

Val Tyr Glu Ala Asn Gly Met Ile Leu His Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Val Tyr Glu Ala Gly Asp Ile Ile Leu His Leu  
1 5 10

---

(2) INFORMATION FOR SEQ ID NO: 156:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

Val	Arg	Glu	Asp	Asn	His	Leu	Arg	Cys	Trp	Met	Ala	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 157:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

Val	Arg	Glu	Asn	Asn	Ser	Ser	Arg	Cys	Trp	Met	Ala	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 158:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

Ile	Arg	Glu	Gly	Asn	Ile	Ser	Arg	Cys	Trp	Val	Leu	Pro
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 159:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Glu	Asn	Ser	Ser	Gly	Arg	Phe	His	Cys	Trp	Ile	Pro	Ile
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

Glu	Arg	Ser	Gly	Asn	Arg	Thr	Phe	Cys	Trp	Thr	Ala	Val
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Glu	Leu	Gln	Gly	Asn	Lys	Ser	Arg	Cys	Trp	Ile	Pro	Val
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Glu Arg His Gln Asn Gln Ser Arg Cys Trp Ile Pro Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

Glu Trp Lys Asp Asn Thr Ser Arg Cys Trp Ile Pro Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Glu Arg Glu Gly Asn Ser Ser Arg Cys Trp Ile Pro Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Val Arg Glu Gly Asn Gln Ser Arg Cys Trp Val Ala Leu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 166:

---

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Val	Arg	Thr	Gly	Asn	Gln	Ser	Arg	Cys	Trp	Val	Ala	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

Val	Arg	Val	Gly	Asn	Gln	Ser	Ser	Cys	Trp	Val	Ala	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

Val	Arg	Val	Gly	Asn	Gln	Ser	Arg	Cys	Trp	Val	Ala	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Val	Lys	Glu	Gly	Asn	His	Ser	Arg	Cys	Trp	Val	Ala	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Val	Lys	Thr	Gly	Asn	Thr	Ser	Arg	Cys	Trp	Val	Ala	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Ile	Lys	Ala	Gly	Asn	Glu	Ser	Arg	Cys	Trp	Leu	Pro	Val
1				5					10			

(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

---

Val Lys Xaa Xaa Asn Gln Ser Arg Cys Trp Val Gln Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Val Lys Thr Gly Asn Leu Thr Lys Cys Trp Leu Ser Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

Val Arg Ser Gly Asn Thr Ser Arg Cys Trp Ile Pro Val  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

Val Lys Asn Ala Ser Val Pro Thr Ala Ala  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:



- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

Val	Lys	Asp	Ala	Asn	Val	Pro	Thr	Ala	Ala
1				5					10

(2) INFORMATION FOR SEQ ID NO: 177:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

Ala	Arg	Ile	Ala	Asn	Ala	Pro	Ile	Asp	Glu
1				5					10

(2) INFORMATION FOR SEQ ID NO: 178:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

Val	Ser	Lys	Pro	Gly	Ala	Leu	Thr	Lys	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

Val	Ser	Arg	Pro	Gly	Ala	Leu	Thr	Arg	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

Val	Asn	Gln	Pro	Gly	Ala	Leu	Thr	Arg	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Val	Ser	Gln	Pro	Gly	Ala	Leu	Thr	Arg	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Val	Ser	Gln	Pro	Gly	Ala	Leu	Thr	Lys	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 183:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

Val	Ser	Arg	Pro	Gly	Ala	Leu	Thr	Glu	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 184:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Ala	Pro	Tyr	Ile	Gly	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 185:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Ala	Pro	Tyr	Thr	Ala	Ala	Pro	Leu	Glu	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Ala	Pro	Ile	Leu	Ser	Ala	Pro	Leu	Met	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Val	Pro	Asn	Ser	Ser	Val	Pro	Ile	His	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

Val	Pro	Asn	Ala	Ser	Thr	Pro	Val	Thr	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

---

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Val	Gln	Asn	Ala	Ser	Val	Ser	Ile	Arg	Gly
1				5					10

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

Val	Lys	Ser	Pro	Cys	Ala	Ala	Thr	Ala	Ser
1				5					10

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

Ser	Pro	Arg	Met	His	His	Thr	Thr	Gln	Glu
1				5					10

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Ser	Pro	Arg	Leu	Tyr	His	Thr	Thr	Gln	Glu
1				5					10

(2) INFORMATION FOR SEQ ID NO: 193:

---

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Thr	Ser	Arg	Arg	His	Trp	Thr	Val	Gln	Asp
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Ala	Pro	Lys	Arg	His	Tyr	Phe	Val	Gln	Glu
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 195:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Ser	Pro	Gln	Tyr	His	Thr	Phe	Val	Gln	Glu
1				5				10	

(2) INFORMATION FOR SEQ ID NO: 196:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

Ser	Pro	Gln	His	His	Asn	Phe	Ser	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

Ser	Pro	Gln	His	His	Ile	Phe	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

Ser	Pro	Glu	His	His	His	Phe	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

---

Arg Pro Arg Arg His Trp Thr Thr Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 200:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

Arg Pro Arg Arg His Trp Thr Ala Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

Gln Pro Arg Arg His Trp Thr Thr Gln Asp  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 202:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 10 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

Arg Pro Arg Arg His Trp Thr Thr Gln Glu  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 203:

- (i) SEQUENCE CHARACTERISTICS:



(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

Gln	Pro	Arg	Arg	His	Trp	Thr	Val	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

Arg	Pro	Lys	Tyr	His	Gln	Val	Thr	Gln	Asp
1				5					10

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

Arg	Pro	Arg	Met	His	Gln	Val	Val	Gln	Glu
1				5					10

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Arg	Pro	Arg	Met	Tyr	Glu	Ile	Ala	Gln	Asp
1			5					10	

(2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

Arg	His	Arg	Gln	His	Trp	Thr	Val	Gln	Asp
1			5					10	